

DR Genew; HGNC:6722; LU.  
 DR MIM: 111200; -.  
 DR GO: GO:0005987; C: integral to plasma membrane; TAS.  
 DR GO: GO:0004888; F: transmembrane receptor activity; TAS.  
 DR GO: GO:0007155; P: cell adhesion; TAS.  
 DR GO: GO:0007165; P: signal transduction; TAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003598; IG\_c2.  
 DR Pfam: PF00047; Ig; 5.  
 DR SMART: SM00408; IGC2; 2.  
 DR PROSITE: PS50835; IG-LIKE; 5.  
 DR Receptor; Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;  
 KW Repeat; Blood group antigen.  
 FT SIGNAL 1 31  
 FT CHAIN 32 628 LUTHERAN BLOOD GROUP GLYCOPROTEIN.  
 FT DOMAIN 32 547 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 548 568 POTENTIAL.  
 FT DOMAIN 569 628 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 32 142 IG-LIKE V-TYPE 1.  
 FT DOMAIN 147 257 IG-LIKE V-TYPE 2.  
 FT DOMAIN 274 355 IG-LIKE C2-TYPE 1.  
 FT DOMAIN 363 441 IG-LIKE C2-TYPE 2.  
 FT DOMAIN 448 541 IG-LIKE C2-TYPE 3.  
 FT DISULFID 53 125 PROBABLE.  
 FT DISULFID 172 237 PROBABLE.  
 FT DISULFID 291 337 PROBABLE.  
 FT DISULFID 384 424 PROBABLE.  
 FT DISULFID 473 522 PROBABLE.  
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 377 377 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 225 226 EL -> DV (IN REF. 2).  
 FT CONFLICT 355 356 EL -> DV (IN REF. 2).  
 SQ SEQUENCE 628 AA; 67374 MW; C69B0X4835492B1E CRC64;  
 . Query Match 7.3%; Score 96; DB 1; Length 628;  
 Best Local Similarity 24.1%; Pred. No. 6.6;  
 Matches 66; Conservative 33; Mismatches 89; Indels 86; Gaps 16;  
 QY 32 KKGDVETLTASQKSIQFMKNSNQIKLGNQGSFLTQSPKLNBRADSRSLMDQGN 91  
 Db REGTVOQLCGDQSPSEPTL-----FRLQDQEVLANVNEGN 321  
 QY 92 PFLIIKQIKEDSDTYICEVE--DQKEVQV--LVFGLTNSDTHLLQGSLLTLESP 146  
 Db --LTLEGVTRGQSGTYGCRVEDYDAADVQSKTLELRVAVLDPLEISEGKVLSTL---P 375  
 QY 147 RGSPPVQC-----RSPRGKNIQGGKTLVSQLELDQSGTTC-----TV 186  
 Db 376 LNSSAVNCSVHGLPTPALRTKSTPLG---DQPMLSLSITFDSNGTYVCCASLPTV 431  
 QY 187 -----LQV-----QKVEFK-IDIVPRAS-----ALPAPTGSALPDPOTA-SALP 225  
 Db 432 PVLSTQNFITLVQGSPELKTAEIEPKADGSGWRGDEVTLICARGH--PDPKLSWSQLG 489  
 QY 226 DPNASALPALAVISFLGLGL-----GVAC 252  
 Db 490 GSP-AEPIPRGQGWVSSLLTKVTSAISRDISC 522  
 RESULT 94  
 VGR3\_MOUSE STANDARD; PRT; 1363 AA.  
 AC P35917;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)  
 DE (VEGF-3) (Tyrosine-protein kinase receptor FLT4).  
 GN FLT4 OR FLT-4.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6J;  
 RX MEDLINE=9330572; PubMed=8393164;  
 RA Finerly H., Kelleher K., Morris G.E., Bean K., Merberg D.M.,  
 RA Kitz R., Morris J.C., Sockdeo H., Turner K.J., Wood C.R.,  
 RT "Molecular cloning of murine FLT and FLT4."  
 RL Oncogene 8:2293-2298(1993).  
 CC -1- FUNCTION: RECEPTOR FOR VEGF-C. HAS A TYROSINE-PROTEIN KINASE  
 CC ACTIVITY.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADULT LUNG AND LIVER, AND IN  
 CC FETAL LIVER, BRAIN, INTESTINE AND PLACENTA.  
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases.  
 CC CSF-1/POGF receptor subfamily.  
 CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.  
 CC -----  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 DR EMBL: L07296; AAA0077.1; -.  
 DR PIR: I58375; I58375.  
 DR HSP; P11362; IREG.  
 DR MGD; MGI:95561; Flc4.  
 DR GO: GO:0005515; F: protein binding; IPI.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003598; IG\_c2.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR001824; ReceptcyrkinsIII.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR InterPro: IPR008266; Tyr\_pkinase\_AS.  
 DR Pfam: PF00047; Ig; 5.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 2.  
 DR SMART: SM00408; IGC2; 2.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS50835; IG-LIKE; 5.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE: PS00240; RECEPTOR TYR\_KIN\_III; 1.  
 DR Transferrase; Tyrosine-protein kinase; phosphorylation; ATP-binding;  
 KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat;  
 KW Glycoprotein.  
 FT SIGNAL 1 24  
 FT CHAIN 25 1363  
 FT DOMAIN 25 775  
 FT TRANSMEM 776 797  
 FT DOMAIN 798 1363  
 FT DOMAIN 44 118  
 FT DOMAIN 151 213  
 FT DOMAIN 230 326  
 FT DOMAIN 331 415  
 FT DOMAIN 422 552  
 FT DOMAIN 555 671  
 FT DOMAIN 678 764  
 FT DOMAIN 845 1173  
 FT NP\_BIND 851 859  
 FT BINDING 879 879  
 FT ACT\_SITE 1037 1037  
 FT DISULFID 51 111  
 FT DISULFID 158 206  
 . VASCULAR ENDOTHELIAL GROWTH FACTOR  
 RECEPTOR 3.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).  
 IG-LIKE C2-TYPE 1.  
 IG-LIKE C2-TYPE 2.  
 IG-LIKE C2-TYPE 3.  
 IG-LIKE C2-TYPE 4.  
 IG-LIKE C2-TYPE 5.  
 IG-LIKE C2-TYPE 6.  
 IG-LIKE C2-TYPE 7.  
 PROTEIN KINASE.  
 ATP (BY SIMILARITY).  
 ATP (BY SIMILARITY).  
 BY SIMILARITY.  
 POTENTIAL.  
 POTENTIAL.

Query	Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
Qy	33 KGDIVELTCTASQKKSIOFHFKNSQKILNGQS-----PLTKPSPKLNDRAD	7.3%;	Score 95.5;	DB 1;	Length 1363;		
Db	570 EGQGVRLSCRADNYTEHRLRWYRLNLSTLHDAQGNPLLDCKNVLFTPLPEANLEABEP	22.7%;	Pred. No. 19;				
Oy	82 SRSLSMDQGNPPLIKNLKIEDSPTYICEVDEKOE-----VQLVFGLTANSDT						
Db	630 GAR----HATISLNIIPRYAPBEDGYCEVDQRKSQDGHCHKYLSVALAPRLTONLT						
Oy	132 HLLOGQSILTLTLESPPGSS--PS-VOCSPSPKNIQGG-----KTLVSQLELDQSGT						
Db	686 DLIVNVSLSLMRCQVGAHVPSLYWYDERDLLEKESITDLADSNQRLSIRGVREEDDGR						
Oy	182 WTCIV 186						
Db	746 YLCSV 750						
RESULT 95							
ID	NEOI_MOUSE	STANDARD;	PRT;	1493	AA.		
AC	P97798;						
DT	16-OCT-2001 (Rel. 40, Created)						
DT	16-OCT-2001 (Rel. 40, Last sequence update)						
DT	10-OCT-2003 (Rel. 42, Last annotation update)						
DE	Neogenin precursor.						
GN	NEOI OR NGN.						
OS	Mus musculus (Mouse).						
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;						
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX	NCBI_TaxId=10090;						
RN	[1]						
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.						
RC	TISSUE=Brain;						
RX	MEDLINE=97407661; PubMed=9264410;						
RA	Keeling S.L., Gad J.M., Cooper H.M.;						
RT	"Mouse neogenin, a DCC-like molecule, has four splice variants and is						
RT	expressed widely in the adult mouse and during embryogenesis.";						
RL	Oncogene 15:691-700(1997).						
CC	-1- FUNCTION: May be involved as a regulatory protein in the						
CC	transition of undifferentiated proliferating cells to their						
CC	differentiated state. May also function as a cell adhesion						
CC	molecule in a broad spectrum of embryonic and adult tissues.						
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.						
CC	-1- ALTERNATIVE PRODUCTS:						
CC	Event=Alternative splicing; Named isoforms=5;						
CC	Comment=Additional isoforms seem to exist;						
CC	Name=1;						
CC	Isoid=P97798-1; Sequence=Displayed.						
CC	Name=2;						

CC		Isoid=d=p97798-2; Sequence=VSP_002594;
CC	Name=3;	
CC	Isoid=d=p97798-3; Sequence=VSP_002595;	
CC	Note=Expression developmentally regulated;	
CC	Name=4;	
CC	Isoid=d=p97798-4; Sequence=VSP_002596;	
CC	Note=Expression developmentally regulated;	
CC	Name=5;	
CC	Isoid=d=p97798-5; Sequence=VSP_002597;	
CC	Note=Expression developmentally regulated;	
CC	-1- TISSUE SPECIFICITY: Widely expressed.	
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED UBIGUOUSLY THROUGHOUT THE MID TO LATE STAGES OF GESTATION AND IN ADULT TISSUES. STRONG EXPRESSION IS OBSERVED IN THE VENTRAL REGION OF THE VENTRICULAR ZONE OF THE E15.5 MOUSE NEURAL TUBE, AS WELL AS IN THE VENTRICULAR ZONES OF THE MESENCEPHALON AND RHOMENCEPHALON. ISOFORMS 3 AND 4 ARE EXPRESSED AT HIGHER LEVEL COMPARED TO OTHER ISOFORMS E11.5 AND E16.5.	
CC	-1- SIMILARITY: Belongs to the immunoglobulin superfamily. DCC family.	
CC	-1- SIMILARITY: Contains 4 Immunoglobulin-like C2-type domains.	
CC	-1- SIMILARITY: Contains 6 fibronectin type III domains.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb.ch/announce/">http://www.isb.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC	-----	
DR	EMBL; Y09535; CAAT0727.1; .	
DR	HSSP; P02751; ITTF.	
DR	MGD; MG1; I097159; Neol.	
DR	InterPro; IPRO08957; FN_III-like.	
DR	InterPro; IPRO03961; FN_III.	
DR	InterPro; IPRO03963; FNIII subd.	
DR	InterPro; IPRO07110; Ig-like.	
DR	InterPro; IPRO03598; Ig_c2.	
DR	Pfam; PF00041; fn3; 6.	
DR	Pfam; PF00047; Ig; 4.	
DR	PRINTS; PR00014; FNTYPEII.	
DR	SMART; SMO0060; FN3; 6.	
DR	SMART; SMO0408; IGc2; 4.	
KW	PROSITE; PS50835; IG_LIKE; 4.	
KW	Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain; Glycoprotein; Alternative splicing.	
KW	SIGNAL	
FT	CHAIN	1 36 POTENTIAL. NEOGENIN. EXTRACELLULAR (POTENTIAL). CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE 1. IG-LIKE C2-TYPE 2. IG-LIKE C2-TYPE 3. IG-LIKE C2-TYPE 4. FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2. FIBRONECTIN TYPE-III 3. FIBRONECTIN TYPE-III 4. FIBRONECTIN TYPE-III 5. FIBRONECTIN TYPE-III 6. POLY-VAL. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.
FT	DONAIN	37 1493
FT	DONAIN	37 1136
FT	TRANSMEM	1137 1157
FT	DONAIN	1158 1493
FT	DONAIN	63 158
FT	DONAIN	163 249
FT	DONAIN	254 347
FT	DONAIN	352 437
FT	DONAIN	467 564
FT	DONAIN	567 660
FT	DONAIN	661 760
FT	DONAIN	766 860
FT	DONAIN	881 981
FT	DONAIN	982 1083
FT	DONAIN	1149 1153
FT	DISULFD	85 140
FT	DISULFD	184 232
FT	DISULFD	281 331
FT	DISULFD	373 421
FT	CARBOHYD	84 84
FT	CARBOHYD	221 221
FT	CARBOHYD	337 337
FT	CARBOHYD	501 501
FT	CARBOHYD	520 520
FT	CARBOHYD	670 670
FT	CARBOHYD	746 746

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FT CARBOHYD 940 940 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VASPLIC 442 461 Missing (in isoform 2).
FT VASPLIC 863 878 Missing (in isoform 3).
FT VASPLIC 1086 1096 Missing (in isoform 4).
FT VASPLIC 1279 1331 Missing (in isoform 5).
FT VASPLIC 1493 AA; 163159 MW; 441DE919D5E17C0E CRC64;
SEQUENCE 1493 AA; 163159 MW; 441DE919D5E17C0E CRC64;

Query Match 7.3%; Score 95.5; DB 1; Length 1493;
Best Local Similarity 25.0%; Pred. No. 21;
Matches 72; Conservative 29; Mismatches 94; Indels 93; Gaps 17;

QY 10 LLLVQLALPAA-----TQGNKV-----VLKGGDTVELT 40
DB 25 LLLVQLALPAAATKSGPRRSGASVTFPPFVLEPVDTLSRGSSVILN 84
QY 41 CTASQKSIQFMKNSNIGKLGNGSFLTKGPKSLNRADSRSLMDQGNFLLIKL 99
DB 85 CSAVSESPNIEWK-----KDGTF-----LNLESDDRQLPDSG--LFTSNV 126
QY 100 ----KIEBSPDYIC--EVED-----QKEVQLVFEGL-----TANSDTHLQGSILTLLES 145
DB 127 HSKNNKPEBPGYQCACATVDNIGTIVSRRAKLTVALGPRFTQPESSVYVGNAILNCEV 186
QY 146 PRGSSPSV---QCSNP-----RGKNIQGGKTLVSQLELQDSGTWTC-----184
DB 187 NADLVPEFVRWQGNQPLLDLRIVLPDGL--TLVISNATEGGCGYRCIVESGCPPEKFSDE 245
QY 185 ---TYLQNKQKVEPRIDIV--PRASALPAPPTGSLPPPPQASALPDP 227
DB 246 AELKVLQDPEEI---VDLVLMRPSM--MKVTGQSAVLPCVSGLPAP 289

RESULT 96
FCBL_RAT STANDARD; PRT; 245 AA.
ID FCBL_RAT PRT; 245 AA.
AC P12371;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE (FEER1) (IG_EFC_receptor, alpha-subunit) (FC-epsilon RI-alpha).
GN FCER1A OR FCBLA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=88024987; PubMed=2959318;
RT "A cDNA presumptively coding for the alpha subunit of the receptor
RT with high affinity for immunoglobulin E."
RL Biochemistry 26:4605-4610(1987).
RN (2)
RP REVISIONS.
RA Kochan J.;
RL Submitted (MAR-1988) to the EMBL/Genbank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RP TISSUE=mast cells;
RX MEDLINE=88158102; PubMed=2964640;
RA Shimizu A., Tepler I., Bentley P.N., Berenstein E.H., Stragman R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
RN (4)
RP SEQUENCE OF 21-245 FROM N.A.
RX MEDLINE=88289772; PubMed=2969594;

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RA Liu F.-T., Albrandt K., Robertson M.W.;
RT "cDNA heterogeneity suggests structural variants related to the high-
RT affinity IGE receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643(1988).
CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
CC -1- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC DISULFIDE LINKED GAMMA CHAINS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC
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CC
DR EMBL; M17153; AAA42045.1; -
DR EMBL; J03606; AAA41582.1; -
DR EMBL; M21622; AAA41146.1; -
DR PIR; G31327; A30154.
DR HSSP; P12319; IALS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG; 2.
DR SMART; SMO0409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 1.
KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT FT SIGNAL 1 23
FT CHAIN 24 245
FT DOMAIN 24 204 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT TRANSMEM 205 223 RECEPTOR ALPHA-SUBUNIT.
FT DOMAIN 224 245 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 28 103 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 113 181 IG-LIKE 1.
FT DISULFID 49 91 IG-LIKE 2.
FT DISULFID 130 174 BY SIMILARITY.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 245 AA; 27793 MW; A0E67DD363872197 CRC64;

Query Match 7.2%; Score 95; DB 1; Length 245;
Best Local Similarity 23.4%; Pred. No. 2.5;
Matches 50; Conservative 32; Mismatches 66; Indels 66; Gaps 10;

QY 11 LLLVQLALPAAATGKRVVLEK-----KQDTVELTC---TASQKSIQFMKNSNOIKI 61
DB 13 LVLSLQVLMATNOKSVSLDPPWIRLTLDKVTLLCNGNNSQGMNSTK--WINDSI-- 68
QY 62 LGNGSFLTKGPKSLNRADSRSLMDQGNFLLIKLKIEDSPDYICEVD--QKEVQ 119
DB 69 -----SNVKSQHW-----VIVATITQDSGKYICQKGFYKSPVY 103
QY 120 LTVFGLTANSDTHLQGSILTLTESPPGSSPSVQSGPPG-----KNIQ 164
DB 104 LNVW-----QEWLLQSSADVLDN---GSPDRGSSMKMKVKHXYIKDDIAFYKSY 154
QY 165 GSKTLVSQLELQDSGTWTCITVLQNKQKVEFKID 198
DB 155 DSNNISIRKATFNDGSGYHCTGYLN--KVECKSD 186

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RESULT 97
VGR2_HUMAN STANDARD; PRT; 1356 AA.
ID VGR2_HUMAN
AC P35968; 060723; Q14178;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VEGFR-2) (kinase insert domain receptor) (Protein-tyrosine kinase
DE receptor Flk-1).
DE KDR OR FLK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin L.Y., Wu Y., Patterson C.;
RT "Full length human KDR/Flk-1 sequence.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RA Shows T.B.;
RT "Identification of a new endothelial cell growth factor receptor
RT tyrosine kinase.";
RL Oncogene 6:1677-1683 (1991).
RN [4]
RP SEQUENCE OF 1-22 FROM N.A.
RX MEDLINE=96032749; PubMed=7559454;
RA Patterson C., Perrella M.A., Hsieh C.M., Yoshizumi M., Lee M.E.,
RA Harber E.;
RT "Cloning and functional analysis of the promoter for KDR/Flk-1, a
RT receptor for vascular endothelial growth factor.";
RL J Biol. Chem. 270:23111-23118 (1995).
RN [5]
RP FUNCTION:
RX MEDLINE=93038639; PubMed=1417831;
RA Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D.,
RA Armellino D.C., Gospodarowicz D., Boehlen P.;
RT "Identification of the KDR tyrosine kinase as a receptor for vascular
RT endothelial cell growth factor.";
RL Biochem. Biophys. Res. Commun. 187:1579-1586 (1992).
CC -1- FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN
CC KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTEM
CC PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF
CC VASCULAR PERMEABILITY.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases.
CC CSF-1/PDGF receptor subfamily.
CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL; AF035121; AAB88005.1; -.

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DR EMBL; AF063658; AAC16450.1; -.
DR EMBL; X61656; CAA43837.1; -.
DR EMBL; L04947; AAB59459.1; -.
DR EMBL; X89776; CAA61916.1; -.
DR PIR; JCI402; JCI402.
DR HSSP; P11362; 1FGK.
DR Genew; HGNC:6307; KDR.
DR MIM; 191306; -.
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0005021; F: vascular endothelial growth factor receptor; TAS.
DR GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. .; TAS.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR01824; RecepttyrkinaIII.
DR InterPro; IPR01245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_pkinase_As.
DR Pfam; PF00047; Ig; 6.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; Igc2; 2.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
DR KEGG; Angiogenesis; Signal; Transferase; Tyrosine-protein kinase; Receptor;
DR KEGG; Transmembrane; Glycoprotein; Phosphorylation; ATP-binding;
DR KEGG; Immunoglobulin domain; Repeat.
DR KEGG; CHAIN 1 19
DR KEGG; CHAIN 20 1356
DR FT DOMAIN 20 764
DR FT TRANSMEM 765 789
DR FT DOMAIN 790 1356
DR FT DOMAIN 141 207
DR FT DOMAIN 224 320
DR FT DOMAIN 328 414
DR FT DOMAIN 421 548
DR FT DOMAIN 551 660
DR FT DOMAIN 667 753
DR FT DOMAIN 834 848
DR FT NP_BIND 848 868
DR FT BINDING 868 868
DR FT ACT_SITE 1028 1028
DR FT CARBOHYD 46 46
DR FT CARBOHYD 66 66
DR FT CARBOHYD 96 96
DR FT CARBOHYD 143 143
DR FT CARBOHYD 158 158
DR FT CARBOHYD 245 245
DR FT CARBOHYD 318 318
DR FT CARBOHYD 374 374
DR FT CARBOHYD 395 395
DR FT CARBOHYD 511 511
DR FT CARBOHYD 523 523
DR FT CARBOHYD 580 580
DR FT CARBOHYD 613 613
DR FT CARBOHYD 619 619
DR FT CARBOHYD 631 631
DR FT CARBOHYD 675 675
DR FT CARBOHYD 704 704
DR FT CARBOHYD 721 721
DR FT MOD_RES 1059 1059
DR FT CONFLICT 2 2
DR FT CONFLICT 772 772
DR FT CONFLICT 787 787
DR FT CONFLICT 835 835
DR FT CONFLICT 848 848
DR FT CONFLICT 1347 1347
DR SO SEQUENCE 1356 AA; 151526 MM; 59E7C44B05CEBB3 CRC64;

```



Page : 1

Query Match Similarity 7.2% Score 94.5; DB 1, Length 108, Gaps 3,  
Pred. No 0.99; 53; Indels 9;  
Best Local Similarity 33.0%; 7; Mismatches 82  
Matches 34; Conservative

QY :  
DB :  
CG :  
61

TGCKNVVAGKKGVTELTCTASOKKSLQPHWKNNSQIKITLGNQSFLLTKGPSKYLNRAHS 82  
5 TQSPSSLSASVGDNRVTITCOASODISIFLWNOCKP---GAKPKLLIADSKACVGS 60  
83 RRLVMDOG-NFPLILTKLKIEDSDTYTICEVDKEVOLLYLV 124  
RFGSTGSGTDFTFLISSLPEDIRATYICQDNLNPF---LTFG 99

RESULT 99 STANDARD; PRT: 210 AA.

CDBB-PONBY CDBB-PONFY  
P30434; Rel. 25, Created (Antigen CDBB)  
01-APR-1993 (Rel. 25, Last annotation update)  
01-APR-1993 (Rel. 42, Last chain precursor)  
10-OCT-2003 (Rel. 42, Last chain precursor)  
CDBB.  
Pongo pygmaeus (Orangutan).  
Eukaryota; Metazoa; Chordata; Catarrhini; Hominoidea; Pongidae.  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongidae.  
NCBI Taxid=9600:  
[ ] -SEQUENCE FROM N.A.  
STRAIN=Isolate Jari; PubMed=1612644;  
MEDLINE=9237742; Parham P.;  
Lawlor D.A., of CD8 alpha and beta chains of the orangutan novel  
structure of mRNA splicing cytochrome c/suppressor T-cells that interact in  
patterns of 36:121-125 (1992).  
Immunogenetics identifies cytotoxic CD8 is thought to play a role in  
with MHC class I bearing targets.  
FUNCTION: Identifies cytotoxic CD8 is thought to play a role in  
the process of T-cell mediated killing.  
SUBUNIT: In general heterodimer of an alpha and a beta chain  
linked by two disulfide bonds.  
LINKED WITH LOCATIONS: Type I membrane protein.  
ALTERNATIVE PRODUCTS: Named isoforms are produced. Alternative splicing  
Event=Alternative number of the hinge or cytoplasmic domains.  
Comment=Excision of the hinge or cytoplasmic domains.  
Name=P30434-1; Sequence=Displayed:  
IsoId:P30434-1; Contains 1 immunoglobulin-like V-type domain.  
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation  
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or send an email to license@isb-sb.ch.

CAIA2783.1;  
EMBL; X60222; S25657.  
DR PIR: S25657; C.T-cell receptor activity; ISS.  
DR GO: GO:0042101; F:coreceptor activity; ISS.  
DR GO: GO:0015026; F:MHC class I protein binding; ISS.  
DR GO: GO:0042288; F:protein binding; ISS.  
DR GO: GO:0005515; F:pigment response; ISS.  
DR GO: GO:0006955; P:immune response; ISS.  
DR GO: GO:0042119; P:T-cell activation; ISS.  
DR GO: GO:0007160; P:transmembrane receptor protein tyrosine kin. .; ISS.  
DR InterPro: IPRO03599; IG-like.  
DR InterPro: IPRO03599; IG-like.  
DR Pfam: PF00047; IG\_1.  
DR SMART: SM00409; IG\_1.  
DR PROSITE: PS50845; IG like: 1.  
DR Immunoglobulin domain; Transmembrane; T-cell; Antigen; Glycoprotein,  
Immune response; Signal; Alternative splicing.  
KW IMMUNOGLOBULIN DOMAIN BY SIMILARITY.  
FT SIGNAL 21

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FT CHAIN 22 210 T-CELL SURFACE GLYCOPROTEIN CD8 BETA
FT DOMAIN 22 170 CHAIN
FT TRANSMEM 171 191 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 192 210 POTENTIAL.
FT DOMAIN 22 123 CYTOPLASMIC (POTENTIAL).
FT DISUFID 41 116 IG-LIKE V-TYPE.
SQ SEQUENCE 210 AA; 23693 MW; F455B0F281C73DC1 CRC64;

Query Match 7.2%; Score 94.5; DB 1; Length 210;
Best Local Similarity 25.7%; Pred. No. 2.2;
Matches 45; Conservative 23; Mismatches 72; Indels 35; Gaps 8;

QY 10 LLLVQLALL-----PA--ATGKNVYLCKGDTVLTCTAS-QKKSIQFHKNS 57
DB 7 LLLAQLAVHSGSSVLOQTDAVYKVNKKVM-----LSCEAKISLNMMIYWROR 58
QY 58 QIKILGNSGFL-----TKGPSKLNDRADRSRLM-DQGNFPLIKLKIEDSDTYICEV 111
DB 59 QATSSDSHHEFLALMDAKTIISEVEQKAVFRASFLINLSVKEDSGIYFCWI 118
QY 112 EDOKEVQVLVFGLTANSSTHLLQGSLTLTSPGSSPSVQ-CSPRGNIQG 165
DB 119 VGSPE-----LTFGKGTQLSVVDPLPTTAOPTKSTPKRRVCRLPREPOTKG 165

RESULT 100
BUT_MOUSE STANDARD; PRT; 524 AA.
ID BUT_MOUSE
AC Q62556; P97392;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Butyrophilin precursor (BT) (Butyrophilin subfamily 1 member A1).
GN BTN1A1 OR BTN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary gland;
RX MEDLINE=97148936; Pubmed=8995761;
RA Ogg S.L., Komargiri M.V.S., Mather I.H.;
RT "Structural organization and mammary-specific expression of the
RT butyrophilin gene."
RL Mamm. Genome 7:900-905(1996).
RN (2)
RP SEQUENCE OF 39-487 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96125723; Pubmed=8541302;
RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;
RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin
RT specifically associates with a 150-kDa protein of mammary epithelial
RT cells and milk fat globule membrane."
RL Biochim. Biophys. Acta 1245:285-292(1995).
CC -FUNCTION: May function in the secretion of milk-fat droplets. It
CC may act as a specific membrane-associated receptor for the
CC association of cytoplasmic droplets with the apical plasma
CC membrane (By similarity).
CC -SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase.
CC -SUBCELLULAR LOCATION: Type I membrane protein.
CC -TISSUE SPECIFICITY: Expressed in mammary tissue and secreted in
CC association with the milk-fat-globule membrane during lactation.
CC -DEVELOPMENTAL STAGE: Expression increases during the last half of
CC pregnancy and is maximal during lactation.
CC -SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG
CC family.
CC -SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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CC -----
CC EMBL; U67065; AAB51034.1; -
CC EMBL; S80642; AAB35893.1; -
CC MGD; MGI:103118; Bttnal.
DR InterPro; IPR001870; B302.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00042; IG; 1.
DR Pfam; PF00627; SPRY; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KM Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.
FT SIGNAL 1 36
FT CHAIN 27 524
FT DOMAIN 27 247
FT TRANSMEM 248 268
FT DOMAIN 269 524
FT DOMAIN 29 141
FT DOMAIN 149 235
FT CARBOHYD 36 56
FT CARBOHYD 216 216
FT CONFLICT 46 46
FT CONFLICT 117 117
FT CONFLICT 191 191
FT CONFLICT 210 210
FT CONFLICT 363 363
FT CONFLICT 408 408
FT CONFLICT 413 414
FT CONFLICT 420 423
FT CONFLICT 492 509
SQ SEQUENCE 524 AA; 58406 MW; 333F4DE2C7704480 CRC64;

Query Match 7.2%; Score 94.5; DB 1; Length 524;
Best Local Similarity 22.3%; Pred. No. 6.9;
Matches 62; Conservative 42; Mismatches 99; Indels 75; Gaps 13;

QY 11 LVLQLALLPAA-----TGANKVYLCKGDTVLTCTASQKSIQF---HKNSQIQT 61
DB 16 LTVLQLPTLDSAPFDVTPAQEPVVALVGSDAELTCGFSPNASEYMWELWFRQTRSTAV 75
QY 62 L-----GNQGSFLT--KGPSKLNDRADRSRLMDQGNFPLIKLKIEDSDTYICEVD 113
DB 76 LLYRDQDEEGQOMTEYRGRATL-----ATAGLID-GRATLIRVDRVADQGEYRCLFND 129
QY 114 ---QKEVQVLVFGLTANSSTHLLQGSLTLTSPGSSPSVQ---SPSVQGRS----- 157
DB 130 NDDFEAAVYLVKAAVGSQDPSQISMTVQENGEMELTSSGWYPEPQVQRTGNREMLPST 189
QY 158 --PRGNIGQKTLVSQLELDG--TWTCIV---LONQKVEKDIIVPAASALPAP 209
DB 190 SEBKKNIEGGLTFVAVSNM-IRDSSTKXNMSCIOWILLQOGKEVEI----- 234
QY 210 PTGSALPDPOTAALPDPPAASALPALAVISFLGLG 247
DB 235 -----SLPAPVPRVLTPIVAVALIILALG 259

Search completed: August 3, 2004, 13:09:18
Job time : 7.54316 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2004, 12:51:44 ; Search time 17.7158 Seconds  
(without alignments)  
4594.975 Million cell updates/sec

Title: SEQ6  
Perfect score: 1317  
Sequence: 1 MNRGVPRRLHLVLQLALP.....VISFLGLGIVACVLARTR 258

Scoring table:  
BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 125 summaries

Database :  
1: SPREMBL\_25:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	767	58.2	397	6	009261 cercoptihc
2	767	58.2	397	6	009262 cercoptihc
3	767	58.2	397	6	009263 cercoptihc
4	767	58.2	397	6	009264 cercoptihc
5	763	57.9	397	6	009259 cercoptihc
6	763	57.9	397	6	009260 cercoptihc
7	758	57.6	397	6	002805 cercoptihc
8	741.5	56.3	457	6	08H2T8 calilitrix
9	740.5	56.2	457	6	08H2T7 calilitrix
10	592	45.0	455	6	09X578 delphinapte
11	557.5	42.3	474	6	P79355 felis alive
12	467	35.5	457	11	061396 mus musculu
13	436.5	33.1	433	11	055054 mus musculu
14	400	30.4	86	6	077596 mandrillus
15	400	30.4	86	6	077597 mandrillus
16	397	30.1	86	6	077594 cercoptihc

17	397	30.1	86	6	077599 theropithec
18	395	30.0	86	6	077595 cercocebus
19	392	29.8	86	6	077598 papio sp. (
20	388	29.5	86	6	077601 lophocebus
21	383	29.1	86	6	077600 lophocebus
22	357	27.1	71	4	013969 homo sapien
23	305.5	23.2	99	6	029027 sus scrofa
24	280.5	21.3	99	6	029028 sus scrofa
25	172	13.1	482	13	090MB5 anas platyr
26	157.5	12.0	538	6	029123 sus scrofa
27	156.5	11.9	538	6	028939 sus scrofa
28	153	11.6	487	13	09W6V7 gallus gall
29	144	10.9	287	11	09D7B8 mus musculu
30	141	10.7	650	6	09GKR2 bos taurus
31	141	10.7	739	6	09GKR3 bos taurus
32	132	10.0	739	6	028260 canis famli
33	131.5	10.0	1496	4	092626 homo sapien
34	131	9.9	955	4	08NFP4 canip4 homo sapien
35	130	9.9	338	4	08IV49 homo sapien
36	130	9.9	1259	11	090Y38 mus musculu
37	129.5	9.8	437	6	08I2P8 homo sapien
38	129	9.8	731	6	08SP16 capre macropus eu
39	126	9.6	341	11	08BLK3 mus musculu
40	125.5	9.5	226	4	013857 homo sapien
41	125.5	9.5	1431	11	080U60 mus musculu
42	125	9.5	332	4	08TA95 homo sapien
43	125	9.5	358	13	08UV81 mus musculu
44	125	9.5	390	4	09HIX9 mus musculu
45	125	9.5	512	4	096DN8 mus musculu
46	125	9.5	545	5	09VCT4 mus musculu
47	125	9.5	5636	4	096RW7 mus musculu
48	124.5	9.5	394	11	09EOK9 mus musculu
49	124.5	9.5	504	13	098823 gallus gall
50	124.5	9.5	584	13	098821 gallus gall
51	124.5	9.5	584	13	090989 gallus gall
52	124.5	9.5	626	13	098922 gallus gall
53	124.5	9.5	626	13	090880 gallus gall
54	124.5	9.5	2828	4	09NRP9 mus musculu
55	124	9.4	325	13	08UV52 mus musculu
56	124	9.4	739	11	063669 mus musculu
57	122.5	9.3	532	5	09VLE0 mus musculu
58	122	9.3	355	4	0723B1 mus musculu
59	122	9.3	1009	13	093250 mus musculu
60	121	9.2	885	6	08HYV1 mus musculu
61	121	9.2	886	6	08HY2 mus musculu
62	120	9.1	1005	13	P79921 xenopus lae
63	120	9.1	1091	11	P70193 mus musculu
64	120	9.1	2222	5	097394 mus musculu
65	119.5	9.1	311	11	09UIM2 mus musculu
66	119	9.0	352	13	09W6V2 mus musculu
67	119	9.0	1395	5	044924 mus musculu
68	118.5	9.0	276	13	08AW79 mus musculu
69	118.5	9.0	278	13	08AW80 mus musculu
70	118.5	9.0	584	4	09Y3Y8 mus musculu
71	118	9.0	348	11	080X24 mus musculu
72	118	9.0	403	5	09VP08 mus musculu
73	118	9.0	577	11	09D221 mus musculu
74	118	9.0	577	11	080Y42 mus musculu
75	118	9.0	1395	5	09W213 mus musculu
76	118	9.0	4117	5	08IRV9 mus musculu
77	118	9.0	4179	5	09W4Y4 mus musculu
78	118	9.0	4223	5	08MPN3 mus musculu
79	118	9.0	6831	5	023550 caenorhabdi
80	118	9.0	7158	5	023551 caenorhabdi
81	117	8.9	350	7	002869 gallus gall
82	117	8.9	811	5	09VNP2 mus musculu
83	117	8.9	1011	5	024273 mus musculu
84	116.5	8.8	192	11	07TD03 mus musculu
85	116.5	8.8	285	4	043608 mus musculu
86	116.5	8.8	359	5	09V6C2 mus musculu
87	116.5	8.8	570	4	08NCB6 mus musculu
88	116.5	8.8	660	4	072681 mus musculu
89	116.5	8.8	739	6	0865F2 mus musculu

```

90 116.5 8.8 1235 4 095428 095428 homo sapien
91 116.5 8.8 1380 4 098CK4 098CK4 homo sapien
92 116 8.8 354 4 08NAQ3 08NAQ3 homo sapien
93 115.5 8.8 484 11 099LA6 099LA6 mus musculu
94 115.5 8.8 820 11 07TPD3 07TPD3 mus musculu
95 115 8.7 344 5 09VY33 09VY33 drosophila
96 114.5 8.7 236 4 0723Y4 0723Y4 homo sapien
97 114.5 8.7 308 13 08UDG3 08UDG3 homo sapien
98 114.5 8.7 2673 4 096SC3 096SC3 homo sapien
99 114 8.7 438 4 0723W6 0723W6 homo sapien
100 114 8.7 2221 5 09UM1 09UM1 drosophila
101 114 8.7 2232 5 086B07 086B07 drosophila
102 114 8.7 2232 5 086B07 086B07 drosophila
103 113.5 8.6 236 13 042404 042404 gallus gall
104 113 8.6 303 13 08UV48 08UV48 brachydantio
105 113 8.6 340 11 088654 088654 mus musculu
106 113 8.6 342 13 091B00 091B00 spheroeides
107 113 8.6 920 4 09P232 09P232 homo sapien
108 113 8.6 1018 6 028106 028106 bos taurus
109 113 8.6 1060 11 09Q213 09Q213 rattus norv
110 113 8.6 1094 4 09B1B8 09B1B8 homo sapien
111 112.5 8.5 280 13 08UV51 08UV51 brachydantio
112 112 8.5 319 11 0922D5 0922D5 mus musculu
113 112 8.5 319 11 09JKA5 09JKA5 mus musculu
114 112 8.5 4228 5 081RV8 081RV8 drosophila
115 111.5 8.5 2053 4 08KXU7 08KXU7 homo sapien
116 111.5 8.5 2053 4 081ZV4 081ZV4 homo sapien
117 111.5 8.5 2113 4 08TD84 08TD84 homo sapien
118 111 8.4 397 11 09JIE0 09JIE0 mus musculu
119 111 8.4 702 4 08N4D0 08N4D0 homo sapien
120 111 8.4 1091 2 006556 006556 streptococ
121 111 8.4 1093 4 096JN1 096JN1 homo sapien
122 110.5 8.4 204 11 09JLM3 09JLM3 rattus norv
123 110.5 8.4 210 11 08R1M4 08R1M4 mus musculu
124 110.5 8.4 329 11 092178 092178 mus musculu
125 110.5 8.4 398 11 007763 007763 mus musculu

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## ALIGNMENTS

```

RESULT 1
009261 PRELIMINARY; PRT; 397 AA.
ID 009261
AC 009261;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD4 (Fragment).
GN CD4.
OS Cercopithecus sabaenus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCB1_Taxid=60711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA Corbet S., Barre-Sinoussi F., Allan J.S.;
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001225; AAB60872.1; -.
DR HSSP; P01730; 1W1Q.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR Pfam; PF00047; Ig_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 397
SQ SEQUENCE 397 AA; 43945 MW; 80C963B92A868CD3 CRC64;
Query Match 58.2%; Score 767; DB 6; Length 397;
Best Local Similarity 85.5%; Pred. No. 1.2e-58;
Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY 28 VVLGKKGDVLELTCTASQKKSIOFHWNKSNQIKILNGQSFLLTKGPKSKLNDRADSRSLW 87
DB 1 VVLGKKGDVLELTCTASQNTTQPFHWNKSNQIKILNGQSFLLTKGSKLRDRIDSRKSLW 60
QY 88 DQGNFLLIKNLIKEDSDRYICEVEQKEVQLVGLTRANSPDTHLLOQSLLTLTLESP 147
DB 61 DQCFSMIIKNLIKEDSEYICEVEKKEVELVGLTRANSPDTHLLOQSLLTLTLESP 120
QY 148 GSSPSVQCRSPRGKNIQGKTLVSQLELDQSGTWCTVLAONQKVEFKIDIV 200
DB 121 GSSPSVQCRSPRGKNIQGKTLVSQLELDQSGTWCTVLAONQKVEFKIDIV 173

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RESULT 2
009262 PRELIMINARY; PRT; 397 AA.
ID 009262
AC 009262;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD4 (Fragment).
GN CD4.
OS Cercopithecus tantalus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCB1_Taxid=60712;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA Corbet S., Barre-Sinoussi F., Allan J.S.;
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001221; AAB60868.1; -.
DR HSSP; P01730; 1W1Q.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 397
SQ SEQUENCE 397 AA; 43954 MW; CF7F2F5D82335B0D CRC64;
Query Match 58.2%; Score 767; DB 6; Length 397;
Best Local Similarity 85.5%; Pred. No. 1.2e-58;
Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
QY 28 VVLGKKGDVLELTCTASQKKSIOFHWNKSNQIKILNGQSFLLTKGPKSKLNDRADSRSLW 87
DB 1 VVLGKKGDVLELTCTASQNTTQPFHWNKSNQIKILNGQSFLLTKGSKLRDRIDSRKSLW 60
QY 88 DQGNFLLIKNLIKEDSDRYICEVEQKEVQLVGLTRANSPDTHLLOQSLLTLTLESP 147
DB 61 DQCFSMIIKNLIKEDSEYICEVEKKEVELVGLTRANSPDTHLLOQSLLTLTLESP 120
QY 148 GSSPSVQCRSPRGKNIQGKTLVSQLELDQSGTWCTVLAONQKVEFKIDIV 200
DB 121 GSSPSVQCRSPRGKNIQGKTLVSQLELDQSGTWCTVLAONQKVEFKIDIV 173

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Dh 121 GSSPSVCKRSPRGKNIQGRITLSVQLERODSGTWTCTVSODONTVEFKIDIV 173
RESULT 3
009263 PRELIMINARY; PRT; 397 AA.
ID 009263
AC 009263;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD4 (Fragment).
GN CD4.
OS Cercopithecus tantalus.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OC NCBI_TaxId=60712;
CX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA Corbet S., Barre-Sinoussi F., Allan J.S.;
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001222; AAB60869.1; -.
DR HSSP; P01730; 1WIO.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 397 AA; 43994 MW; A3CD01535A51524 CRC64;

Query Match 58.2%; Score 767; DB 6; Length 397;
Best Local Similarity 85.5%; Pred. No. 1.2e-58;
Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Dy 28 VILAKKGDVVELTCTASQKSIQPHMKNSNQIKILNGSFLTGPKLNDRAISRSLW 87
Dd 1 VILAKKGDVVELTCTASQNTTQPHMKNSNQIKILNGSFLTGSSKLRDRIDSRKSLW 60
Dy 88 DQGNFPLIKNLKIEDSDTYICEVEDQKEVQLVFGLTANSPTHLQOGSLTTLSP 147
Dd 61 DQGFMSIINKLKIEDSETYICEVENKEEVELLVFGLTANSPTHLQOGSLTTLSP 120
Dy 148 GSSPSVCKRSPRGKNIQGRITLSVQLERODSGTWTCTVSODONTVEFKIDIV 200
Dd 121 GSSPSVCKRSPRGKNIQGRITLSVQLERODSGTWTCTVSODONTVEFKIDIV 173

RESULT 4
009259 PRELIMINARY; PRT; 397 AA.
ID 009259
AC 009259;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD4 (Fragment).
GN CD4.
OS Cercopithecus pygerythrus.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OC NCBI_TaxId=60710;
CX [1]
RN
RP SEQUENCE FROM N.A.
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RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA Corbet S., Barre-Sinoussi F., Allan J.S.;
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001227; AAB60874.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 397 AA; 43946 MW; 21C3E30882ABFC0 CRC64;

Query Match 58.2%; Score 767; DB 6; Length 397;
Best Local Similarity 85.5%; Pred. No. 1.2e-58;
Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Dy 28 VILAKKGDVVELTCTASQKSIQPHMKNSNQIKILNGSFLTGPKLNDRAISRSLW 87
Dd 1 VILAKKGDVVELTCTASQNTTQPHMKNSNQIKILNGSFLTGSSKLRDRIDSRKSLW 60
Dy 88 DQGNFPLIKNLKIEDSDTYICEVEDQKEVQLVFGLTANSPTHLQOGSLTTLSP 147
Dd 61 DQGFMSIINKLKIEDSETYICEVENKEEVELLVFGLTANSPTHLQOGSLTTLSP 120
Dy 148 GSSPSVCKRSPRGKNIQGRITLSVQLERODSGTWTCTVSODONTVEFKIDIV 200
Dd 121 GSSPSVCKRSPRGKNIQGRITLSVQLERODSGTWTCTVSODONTVEFKIDIV 173

RESULT 5
009259 PRELIMINARY; PRT; 397 AA.
ID 009259
AC 009259;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD4 (Fragment).
GN CD4.
OS Cercopithecus sabaesus.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OC NCBI_TaxId=60711;
CX [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA Corbet S., Barre-Sinoussi F., Allan J.S.;
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001223; AAB60870.1; -.
DR HSSP; P01730; 1WIO.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 397 AA; 43881 MW; 7CE39AD0F8506C81 CRC64;
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Query Match 57.9%; Score 763; DB 6; Length 397;  
 Best Local Similarity 85.0%; Pred. No. 2.6e-58;  
 Matches 147; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKGDVTELTCTASOKSIOPHMKNNOIKILGQSFLLTKGPKLNDRADSRSLW 87  
 1 VVLGKGDVTELTCTASOKSIOPHMKNNOIKILGQSFLLTKGSKLDRIDSRSLW 60

QY 88 DQGNFPLIINKLKIEDSDTYICEVEDQKEEVOLLVFGLTANSDTHLLQGSLTTLTLESP 147  
 61 DQGFMSIINKLKIEDSETYICEVENKEEVEVLVFGLTANSDTHLLQGSLTTLTLESP 120

QY 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSGTWTCTVLOQNKVYEFKIDIV 200  
 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSGTWTCTVLOQNKVYEFKIDIV 173

Db 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSGTWTCTVLOQNKVYEFKIDIV 173

RESULT 6  
 ID 009260 PRELIMINARY; PRT; 397 AA.  
 AC 009260;  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE CD4 (Fragment).  
 GN CD4.  
 OS Cercopithecus sabaesus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OC NCBI\_TaxID=60711;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98017879; PubMed=9379478;  
 RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,  
 RA Corbet S., Barre-Sinoussi F., Allan J.S.,  
 RT "Relation between phylogeny of African green monkey CD4 genes and  
 RT their respective simian immunodeficiency virus genes.";  
 RL J. Med. Primatol. 26:120-128(1997).  
 DR EMBL; AF001224; AAB60871.1; -.  
 DR HSSP; P01730; IWIO.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR000973; CD4\_TcAg.  
 DR InterPro; IPR007110; Ig\_Like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_2.  
 DR PRINTS; PR00692; CD4TCANTIGEN.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_Like; 1.  
 DR NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 397 AA; 43882 MW; 478BB277E92EE89 CRC64;

Query Match 57.9%; Score 763; DB 6; Length 397;  
 Best Local Similarity 85.0%; Pred. No. 2.6e-58;  
 Matches 147; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKGDVTELTCTASOKSIOPHMKNNOIKILGQSFLLTKGPKLNDRADSRSLW 87  
 1 VVLGKGDVTELTCTASOKSIOPHMKNNOIKILGQSFLLTKGSKLDRIDSRSLW 60

QY 88 DQGNFPLIINKLKIEDSDTYICEVEDQKEEVOLLVFGLTANSDTHLLQGSLTTLTLESP 147  
 61 DQGFMSIINKLKIEDSETYICEVENKEEVEVLVFGLTANSDTHLLQGSLTTLTLESP 120

QY 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSGTWTCTVLOQNKVYEFKIDIV 200  
 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSGTWTCTVLOQNKVYEFKIDIV 173

Db 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSGTWTCTVLOQNKVYEFKIDIV 173

RESULT 7

002805  
 ID 002805 PRELIMINARY; PRT; 397 AA.  
 AC 002805; 077593;  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3) (Fragment).  
 GN CD4.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OC NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral blood;  
 RX MEDLINE=98017879; PubMed=9379478;  
 RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,  
 RA Corbet S., Barre-Sinoussi F., Allan J.S.,  
 RT "Relation between phylogeny of African green monkey CD4 genes and  
 RT their respective simian immunodeficiency virus genes.";  
 RL J. Med. Primatol. 26:120-128(1997).  
 RN [2]  
 RP SEQUENCE OF 80-165 FROM N.A.  
 RX MEDLINE=98320644; PubMed=9656488;  
 RA Harris E.E., Disocell T.R.;  
 RT "Nuclear gene trees and the phylogenetic relationships of the  
 RT mangabeys (Primates: Papionini).";  
 RL Mol. Biol. Evol. 15:892-900(1998).  
 CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL  
 CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC ONE V-LIKE AND 3 C2-LIKE DOMAINS.  
 DR EMBL; AF001226; AAB60873.1; -.  
 DR EMBL; AF057380; AAC25124.1; -.  
 DR HSSP; P01730; IWIO.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR000973; CD4\_TcAg.  
 DR InterPro; IPR007110; Ig\_Like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_2.  
 DR PRINTS; PR00692; CD4TCANTIGEN.  
 DR SMART; SM00406; IGV; 1.  
 KM Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;  
 KM Lipoprotein; Palmitate; Repeat.  
 FT NON\_TER 1  
 FT DOMAIN <1 370  
 FT TRANSMEM 371 391  
 FT DOMAIN 392 >397  
 FT DOMAIN <1 98  
 FT DOMAIN 99 176  
 FT DOMAIN 177 290  
 FT DOMAIN 291 347  
 FT CARBOHYD 15 15  
 FT CARBOHYD 30 30  
 FT CARBOHYD 269 269  
 FT CARBOHYD 298 298  
 FT DISULFID 14 82  
 FT DISULFID 128 157  
 FT DISULFID 301 343  
 FT LIPID 392 392  
 FT LIPID 395 395  
 FT NON\_TER 397 397  
 SQ SEQUENCE 397 AA; 43980 MW; F74C42E22B196155 CRC64;

Query Match 57.6%; Score 758; DB 6; Length 397;  
 Best Local Similarity 85.0%; Pred. No. 7.1e-58;  
 Matches 147; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

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Qy 28 VLAKGKGTVELTCTASQKSIQFHWKNSNOIKILGNQSGFLTKGSPKLNDRADSRSLM 87
Db 1 VVLGKSGTVELTCTASQKSIQFHWKNSNOIKILGNQSGFLTKGSPKLNDRADSRSLM 60
Qy 88 DQGNFPLIIKNIKIEDSDTYICEVDQKEEVQLVFGLTANSPTLLQSGSLTLTLESP 147
Db 61 DQGNFPLIIKNIKIEDSDTYICEVDQKEEVQLVFGLTANSPTLLQSGSLTLTLESP 120
Qy 148 GSSPSVOCRSRPGKNIQSGKTLVSQLELDQSGTCTVQLNOKKVEFKIDIV 200
Db 121 GSSPSVOCRSRPGKNIQSGKTLVSQLELDQSGTCTVQLNOKKVEFKIDIV 173

RESULT 8
Q8H278 PRELIMINARY; PRT; 457 AA.
ID Q8H278;
AC Q8H278;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Lymphocyte antigen CD4.
OS Callictrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.
NCBI_TaxId=9483;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22174698; PubMed=12186836;
Labonte J.A., Babcock G.J., Patel T., Sodroski J.;
"Blockade of HIV-1 infection of New World Monkey Cells Occurs
Primarily at the Stage of Virus Entry.";
RL J. Exp. Med. 196;431-445(2002).
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000973; CD4_TCAG.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR003596; IG_1v.
DR Pfam; PF00047; IG_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00409; IG; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 457 AA; 50878 MW; 718CFDB78D97F598 CRC64;

Query Match 56.3%; Score 741.5; DB 6; Length 457;
Best Local Similarity 72.5%; Pred. No. 2.4e-56;
Matches 145; Conservative 23; Mismatches 31; Indels 1; Gaps 1;

Qy 1 MNRGVPFRHLLVQLALLPAATGKNVVLGKGDVTELTCTASQKSIQFHWKNSNOIK 60
Db 1 MNGGIPFRHSLVQLALLPAATGKNVVLGKGMVELPCETSLKKKLQFHWKTSNOIK 60
Qy 61 ILGNQSGFLTKGSPKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVDQKEEVQL 120
Db 61 ILGNQSGFLTKGSPKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVDQKEEVQL 120
Qy 121 LVFGLTANSPTLLQSGSLTLTLESPSSPSVOCRSRPGKNIQSGKTLVSQLELDQSG 180
Db 121 QVFGLTANPPTLLQSGSLTLTLESPSSPSVOCRSRPGKNIQSGKTLVSQLELDQSG 180
Qy 181 TWCTCTVQLNOKKVEFKIDIV 200
Db 181 TWKCTVSOHLELV-FKINIV 199

RESULT 9
Q8H277 PRELIMINARY; PRT; 457 AA.
ID Q8H277;
AC Q8H277;
DT 01-MAR-2003 (TREMBlrel. 23, Created)

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DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Lymphocyte antigen CD4.
OS Salimiri beirneus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Salimiri.
NCBI_TaxId=9521;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22174698; PubMed=12186836;
Labonte J.A., Babcock G.J., Patel T., Sodroski J.;
"Blockade of HIV-1 infection of New World Monkey Cells Occurs
Primarily at the Stage of Virus Entry.";
RL J. Exp. Med. 196;431-445(2002).
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000973; CD4_TCAG.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR003596; IG_1v.
DR Pfam; PF00047; IG_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00409; IG; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 457 AA; 50899 MW; B164DA89F70C575A CRC64;

Query Match 56.2%; Score 740.5; DB 6; Length 457;
Best Local Similarity 72.0%; Pred. No. 2.9e-56;
Matches 144; Conservative 24; Mismatches 31; Indels 1; Gaps 1;

Qy 1 MNRGVPFRHLLVQLALLPAATGKNVVLGKGDVTELTCTASQKSIQFHWKNSNOIK 60
Db 1 MNGGIPFRHSLVQLALLPAATGKNVVLGKGMVELPCETSLKKKLQFHWKTSNOIK 60
Qy 61 ILGNQSGFLTKGSPKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVDQKEEVQL 120
Db 61 ILGNQSGFLTKGSPKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVDQKEEVQL 120
Qy 121 LVFGLTANSPTLLQSGSLTLTLESPSSPSVOCRSRPGKNIQSGKTLVSQLELDQSG 180
Db 121 QVFGLTANPPTLLQSGSLTLTLESPSSPSVOCRSRPGKNIQSGKTLVSQLELDQSG 180
Qy 181 TWCTCTVQLNOKKVEFKIDIV 200
Db 181 TWKCTVSOHLELV-FKINIV 199

RESULT 10
Q9XS78 PRELIMINARY; PRT; 455 AA.
ID Q9XS78;
AC Q9XS78;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
NCBI_TaxId=9749;
RX [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Thymus;
MEDLINE=99216435; PubMed=10199913;
Romano T.A., Ridgway S.H., Felten D.L., Quaranta V.;
"Molecular cloning and characterization of CD4 in an aquatic mammal,
the white whale Delphinapterus leucas.";
RL Immunogenetics 49;376-383(1999).
DR EMBL; AF071799; AAD23738.1; -.
DR HSSP; P01730; IWIO.
DR GO; GO:0016020; C:membrane; IEA.

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DR GO:0006955; P:Immune response; IEA.
DR InterPro: IPR000973; CD4 TCAG.
DR InterPro: IPR007110; IG-Like.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_3.
DR PRINTS: PR00692; CD4TCANTIGEN.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR SEQUENCE 455 AA; 50499 MW; AA532FD411AA5D1 CRC64;

Query Match 45.0%; Score 592; DB 6; Length 455;
Best Local Similarity 60.0%; Pred. No. 2.7e-43;
Matches 120; Conservative 24; Mismatches 56; Indels 0; Gaps 0;

OY 1 MNRGVPFHHLLVYQLALLPATGCKNVKLLKKGGDYVLLCTASOKKSIOEHMKNQNIK 60
DB 1 MDPRTSLRHLEFLVLDVLMPLPGTQKKVYLKAGAGELAPCKASQNSLSFPMKNSYOTK 60
OY 61 ILGNQSFLLTGKPSKLANDRARSRLMDQGNFPLIKNLKIEDSPYVICVEDQKEEVQL 120
DB 61 ILGRHGVFMWKGASNLHRSRVESKINLMDQGSFPLVIKQLEVPDSCTYICEVEDKKIEVEL 120
OY 121 LVFGLTANSDPHLLUGOSLTTLTSEPPSSPSVYCRSRGNKIQGGKTLTSQLELDQSG 180
DB 121 QVFRITASSDPRLLLGSLTTLTEGSSNPSSVQMGKGNRKQNEAKSLSLPQVELDQSG 180
OY 181 TWCTCTVLQNKQKVEFKIDIV 200
DB 181 TWCTCTVSQAQCTIVENKHIL 200

RESULT 11
P79355 PRELIMINARY; PRT; 474 AA.
ID P79355
AC P79355
DT 01-MAY-1997 (TREMBLrel. 03. Created)
DT 01-MAY-1997 (TREMBLrel. 03. Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25. Last annotation update)
DE CD4 antigen precursor.
DE CD4 antigen precursor.
DE Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Placentalia; Felidae; Felis.
OX NCBI_TxId=9685;
XP (1)
RP SEQUENCE FROM N.A.
RA Miyazawa T.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=92165316; PubMed=1537604;
RA Northrup J., Miyazawa T., Kawaguchi Y., Tohya Y., Kai C., Mikami T.; of
RT the V-Like region.";
RL Immunology 75:74-79 (1992).
DR EMBL: AB000483; BAA19124.1; -.
DR HSSP: P01730. 1WTO.
DR GO:0016020; C:membrane; IEA.
DR GO:0006955; P:Immune response; IEA.
DR InterPro: IPR00973; CD4 TCAG.
DR InterPro: IPR007110; IG-Like.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_3.
DR PRINTS: PR00692; CD4TCANTIGEN.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 2.
KW Signal.
FT SIGNAL
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 474 POTENTIAL.
SQ SEQUENCE 474 AA; 52243 MW; D946DD4BBAED00EC CRC64;

Query Match 42.3%; Score 557.5; DB 6; Length 474;
Best Local Similarity 55.3%; Pred. No. 3e-40;
Matches 121; Conservative 30; Mismatches 49; Indels 19; Gaps 3

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OY		1	MNRGVPFRHLLVLVQLALLPAAT-OGNKVVJGGKGDVTBELTCTASQOKSIQFHWKNSNOI	59
Dd		1	MNGAFAFRHLLLVQLVLMVKAAVPOGKEVVLGAAGTAELPCAOSQOKWTFTWRLLSSQV	60
OY		60	KILGNQGSFL-TYGPSHLNDRADSRSLMDQGNPPLIKNLKTIEDSDTYICEVEDOKEEV	118
Dd		61	KILESHSSISLCTLGSSSKLTFRFSKKILMDOGSFFPLVIKSLOVADSGIYRCEVENKPREV	120
OY		119	OLIVFGLTANSD-----THLQGOSLTLTLESPSSSVQCRRSRRGK	161
Dd		121	ELLVFGTLAVDVDSGGSGSSSTSTSTSYLLTLTGOSLTLTLESPSSSNPSVOMKPGBNK	180
OY		162	NIOGKTLVSQLELDQSGTWCTCTVLONQKVEFKIDIV	200
Dd		181	SKSGVHSLSLSQLDELQESGTCTCTVSGSQKTLVFNNIL	219
 RESULT 12				
ID	Q61396	PRELIMINARY;	PRT;	457 AA.
AC	Q61396;			
DT	01-NOV-1996	(TREMBL-rel_01, Created)		
DT	01-NOV-1996	(TREMBL-rel_01, Last sequence update)		
DE	01-OCT-2003	(TREMBL-rel_25, Last annotation update)		
DE	T-cell differentiation antigen.			
GN	CD4.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=88041159; PubMed=2823269;			
RX	Gorman S.D., Tourvilleille B., Parnes J.R.;			
RT	"Structure of the mouse gene encoding CD4 and an unusual transcript in			
RL	brain."			
Proc.	Natl. Acad. Sci. U.S.A. 84:7644-7648(1987).			
DR	EMBL; M17080; AAA37402.1; -			
DR	EMBL; M17076; AAA37402.1; JOINED.			
DR	EMBL; M17077; AAA37402.1; JOINED.			
DR	EMBL; M17078; AAA37402.1; JOINED.			
DR	EMBL; M17079; AAA37402.1; JOINED.			
DR	HSSP; P01730; IMBR.			
DR	MGD; MG1:88335; Cd4.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0006955; P:immune response; IEA.			
DR	InterPro; IPR000973; CD4_TCAG.			
DR	InterPro; IPR007110; IG-Like.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF00047; Ig_2.			
DR	PRINTS; PR00692; CD4TCANTIGEN.			
DR	SMART; SM00406; IgV_1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
SQ	SEQUENCE 457 AA; 51368 MW; 24AB19EDA285B5D0 CRC64;			
 Query Match 35.5%; Score 467; DB 11; Length 457; Best Local Similarity 52.3%; Pred. No. 2.3e-32; Matches 103; Conservative 32; Mismatches 56; Indels 6; Gaps 5;				
OY		1	MNRGVPPRH-DLVLQALALPAATOGNKVVJGGKGDVTBELTCTASQOKSIQFHWKNSNOI	59
Dd		1	MCRALSIRLLULLLQLQSLLAVQTIVLGRKGSEAEIPCSSQOKITVFTWKFPDQR	60
OY		60	KILGNQGSFL-TYGPSHLNDRADSRSLMDQGNPPLIKNLKTIEDSDTYICEVEDOKEE	116
Dd		61	KILOHGKGLVLRGSSPSOF-DREDSKKGAMWKSPLINKLMEDSQTYICELRNKE	119
OY		117	EVOLLVGLTPANSDTHLLOGOSLTLTLES-PGSSPVQCRSPRGKNIOGKTLVSQLE	175
Dd		120	EVELVFRKVTFPSPTSLIQGOSLTLTLDDSNSKYSNPLETECHRKKGKXVSGSKVLSMSNR	179
OY		176	LQDSGTWCTCTVLONQK 192	

Db 180 VQSDSFNCTVTLDDCK 196

## RESULT 13

055054 PRELIMINARY; PRT; 433 AA.

AC 055054; (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE T4 surface glycoprotein (Fragment).  
 GN CD4.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NX NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=88097446; PubMed=3501122;  
 RA Madden P.J., Molineux S.M., Madden D.E., Zimmerman K.A., Godfrey M.,  
 Alt F.W., Chess L., Axel R.;  
 RT "Structure and expression of the human and mouse T4 genes";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:9155-9159(1987).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA Madden P.J., Molineux S.M., Madden D.E., Zimmerman K.A., Godfrey M.,  
 Alt F.W., Chess L., Axel R.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF045882; AAC01764.1; -

DR HSSP; P01730; 1MBR.  
 DR MGD; MGI:88335; CD4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR000973; CD4\_TCSG.  
 DR InterPro; IPR007110; IG\_Like.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; Ig\_2.

DR PRINTS; PRO00692; CD4TCANTIGEN.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON TER 1  
 FT NON TER 433  
 SO SEQUENCE 433 AA; 48590 MW; AB19330750A8499A CRC64;

Query Match 33.1%; Score 436.5; DB 11; Length 433;  
 Best Local Similarity 53.2%; Pred. No. 9.9e-30;  
 Matches 92; Conservative 29; Mismatches 47; Indels 5; Gaps 4;

Db 24 OGNKVVIGKGDYELTCTASOKSIOPHMKNSQIKILNQG-SFLTKG--PSKNDRA 80

QY 1 QGKTLVIGKEGSESLPESSQKITVPTWKFSDQKTLGHGKGVLRGSPSQF-DRF 59  
 DB 81 DSRSLMDQGNFPLIKLKIEDSDTYCEVEDQKEEVLVFGLTANSPTHLQGGSLT 140  
 DB 60 DSKGAMKGSFPLINKLKIEDSDTYCEVEDQKEEVLVFGLTANSPTHLQGGSLT 119

QY 141 LTLES-PPGSSPSVQCRSPRGKNIQGGKTLISVSOLELDSGTWTCTVQLQNGK 192  
 DB 120 LTLDNSKVSNPILTECKHKKGKGVSGKVLMSNLRVQSDSFNCTVTLDDCK 172

## RESULT 14

077596 PRELIMINARY; PRT; 86 AA.

AC 077596; (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3) (Fragment).  
 OS Mandrillus sphinx (Mandrill) (Papio sphinx).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Mandrillus.  
 NX NCBI\_TaxID=9561;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=98320644; PubMed=9656488;  
 RA Harris B.E., Disotell T.R.;  
 RT "Nuclear gene trees and the phylogenetic relationships of the  
 mangabeys (primates: Papionini).";  
 RL Mol. Biol. Evol. 15:892-900(1998).

CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL  
 RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY  
 SIMILARITY).

CC -1- SUBUNIT: ASSOCIATES WITH PS6-LCK (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 ONE V-LIKE AND 1 C2-LIKE DOMAIN.

DR EMBL; AF057386; AAC25130.1; -  
 DR HSSP; P01730; 1CDY.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR007110; IG\_Like.  
 DR Immunoglobulin domain; T-cell; MHC; Transmembrane.

FT NON TER 1  
 FT DOMAIN 19 IG-LIKE V-TYPE DOMAIN.  
 FT DOMAIN 20 IG-LIKE C2-TYPE DOMAIN.  
 FT DISUPD 49 BY SIMILARITY.  
 FT NON TER 86

SO SEQUENCE 86 AA; 9406 MW; 2BD97A9EB19582AB CRC64;  
 Query Match 30.4%; Score 400; DB 6; Length 86;  
 Best Local Similarity 89.4%; Pred. No. 1.9e-27;  
 Matches 76; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 107 YICEVEDQKEEVLVFGLTANSPTHLQGGSLTLTSPGSSPSVQCRSPRGKNIQGG 166

DB 1 YICEVEDQKEEVLVFGLTANSPTHLQGGSLTLTSPGSSPSVQCRSPRGKNIQGG 60  
 QY 167 KTLISVSOLELDSGTWTCTVQLQNGK 191  
 DB 61 KTLISVPOLEKDSGTWTCTVSDOK 85

## RESULT 15

077597 PRELIMINARY; PRT; 86 AA.

AC 077597; (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3) (Fragment).

OS Mandrillus leucophaeus (Drill) (Papio leucophaeus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Mandrillus.

CC -1- SUBUNIT: ASSOCIATES WITH PS6-LCK (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 ONE V-LIKE AND 1 C2-LIKE DOMAIN.

DR EMBL; AF057387; AAC25131.1; -  
 DR HSSP; P01730; 1CDY.  
 DR GO; GO:0016021; C:integral to membrane; IEA.

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DR InterPro: IPR007110; Ig-like.
KW Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT NON TER 1
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 49 78 BY SIMILARITY.
FT NON TER 86
SQ SEQUENCE 86 AA; 9406 MW; 2BD97A9EE19582AB CRC64;

Query Match 30.4%; Score 400; DB 6; Length 86;
Best Local Similarity 89.4%; Pred. No. 1.9e-27;
Matches 76; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 107 YICEVEDQKEEVQLVFGLTANSPTHLQGSITLTLESPPGSSPSVQCRSPRGKNIQGG 166
DB 1 YICEVEDKKEVELVFGLTANSPTHLLEGOSITLTLESPPGSSPSVKCRSPRGKNIQGG 60
DB 167 KTLISVQLDELQDSGTWCTCTVLQNOK 191
DB 61 RILSVPOLERODSGTWCTCTVSQDOK 85

RESULT 16
ID 077594 PRELIMINARY; PRT; 86 AA.
AC 077594;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
OS (Fragment).
OC Cercopithecus mitis.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36225;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; PubMed=9656488;
RA Harris E.E., Disocell T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the
RT mangabeys (primates: Papionini).";
RL Mol. Biol. Evol. 15:892-900(1998).
DR HSSP; P01730; 1CDY.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR InterPro: IPR007110; Ig-like.
KW Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT NON TER 1
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 49 78 BY SIMILARITY.
FT NON TER 86
SQ SEQUENCE 86 AA; 9420 MW; 2BD97A98574EB9AB CRC64;

Query Match 30.1%; Score 397; DB 6; Length 86;
Best Local Similarity 89.4%; Pred. No. 3.4e-27;
Matches 76; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 107 YICEVEDQKEEVQLVFGLTANSPTHLQGSITLTLESPPGSSPSVQCRSPRGKNIQGG 166
DB 1 YICEVEDKKEVELVFGLTANSPTHLLEGOSITLTLESPPGSSPSVKCRSPRGKNIQGG 60
DB 167 KTLISVQLDELQDSGTWCTCTVLQNOK 191
DB 61 RILSVPOLERODSGTWCTCTVSQDOK 85

QY 167 KTLISVQLDELQDSGTWCTCTVLQNOK 191
DB 61 RILSVPOLERODSGTWCTCTVSQDOK 85

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RESULT 17
ID 077599 PRELIMINARY; PRT; 86 AA.
AC 077599;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
OS (Fragment).
OC Cercopithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; PubMed=9656488;
RA Harris E.E., Disocell T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the
RT mangabeys (primates: Papionini).";
RL Mol. Biol. Evol. 15:892-900(1998).
DR HSSP; P01730; 1CDY.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR InterPro: IPR007110; Ig-like.
KW Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT NON TER 1
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 49 78 BY SIMILARITY.
FT NON TER 86
SQ SEQUENCE 86 AA; 9420 MW; 2BD97A98574EB9AB CRC64;

Query Match 30.1%; Score 397; DB 6; Length 86;
Best Local Similarity 88.2%; Pred. No. 3.4e-27;
Matches 75; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 107 YICEVEDQKEEVQLVFGLTANSPTHLQGSITLTLESPPGSSPSVQCRSPRGKNIQGG 166
DB 1 YICEVEDKKEVELVFGLTANSPTHLLEGOSITLTLESPPGSSPSVKCRSPRGKNIQGG 60
DB 167 KTLISVQLDELQDSGTWCTCTVLQNOK 191
DB 61 RILSVPOLERODSGTWCTCTVSQDOK 85

QY 167 KTLISVQLDELQDSGTWCTCTVLQNOK 191
DB 61 RILSVPOLERODSGTWCTCTVSQDOK 85

RESULT 18
ID 077595 PRELIMINARY; PRT; 86 AA.
AC 077595;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
OS (Fragment).
OC Cercopithecus galatius chrysogaster.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=75569;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; PubMed=9656488;
RA Harris E.E., Disocell T.R.;

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"Nuclear gene trees and the phylogenetic relationships of the mangabey (primates: Papionini)." ;  
MoJ. Biol. Evol. 15:892-900(1998).  
CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY SIMILARITY).  
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE AND 1 C2-LIKE DOMAIN.  
DR EMBL; AF057382; AAC25126.1; -.  
DR HSSP; P01730; 1CDY.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR InterPro; IPR007110; Ig-like.  
KM Immunoglobulin domain; Glycoprotein; T-cell; MHC; Transmembrane.  
FT NON\_TER 1  
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.  
FT CARBOHYD 20 >86 IG-LIKE C2-TYPE DOMAIN.  
FT DISULFD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT NON\_TER 49 78 BY SIMILARITY.  
FT SEQUENCE 86 86  
SQ SEQUENCE 86 AA; 9419 MW; A9D97A9E19582BE CRC64;  
Query Match 30.0%; Score 395; DB 6; Length 86;  
Best Local Similarity 88.2%; Pred. No. 5.1e-27;  
Matches 75; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
QY 107 YICEVEDQKEVQLLVGLTNSDTHLLQGSLTTLTSPGSSPSVQCSPRGKNIQGG 166  
DB 1 YICEVEDQKEVQLLVGLTNSDTHLLQGSLTTLTSPGSSPSVQCSPRGKNIQGG 60  
QY 167 KTLVSQLELDSDGTWCTVYQONOK 191  
DB 61 RTLSVPOLERQDSGTWCTVNSQDOK 85  
RESULT 19  
QY 077598 PRELIMINARY; PRT; 86 AA.  
AC 077598;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3) (Fragment).  
OS Papio sp. (Baboon).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Papio.  
OX NCBI\_TaxID=61183;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98320644; PubMed=9656488;  
RA Harris E.E., Disotell T.R.;  
RT "Nuclear gene trees and the phylogenetic relationships of the mangabey (primates: Papionini)." ;  
RL MoJ. Biol. Evol. 15:892-900(1998).  
CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY SIMILARITY).  
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE AND 1 C2-LIKE DOMAIN.  
DR EMBL; AF057388; AAC25132.1; -.  
DR HSSP; P01730; 1CDY.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR InterPro; IPR007110; Ig-like.  
KM Immunoglobulin domain; Glycoprotein; T-cell; MHC; Transmembrane.  
FT NON\_TER 1  
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.  
FT CARBOHYD 20 >86 IG-LIKE C2-TYPE DOMAIN.  
FT DISULFD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT SEQUENCE 86 86  
SQ SEQUENCE 86 AA; 9463 MW; 2BD97A88464FBAB CRC64;  
Query Match 29.5%; Score 388; DB 6; Length 86;  
Best Local Similarity 87.1%; Pred. No. 2.1e-26;  
Matches 74; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

FT DISULFD 49 78 BY SIMILARITY.  
FT NON\_TER 86 86  
SQ SEQUENCE 86 AA; 9433 MW; A9D97A9857AEBBE CRC64;  
Query Match 29.8%; Score 392; DB 6; Length 86;  
Best Local Similarity 87.1%; Pred. No. 9.3e-27;  
Matches 74; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 107 YICEVEDQKEVQLLVGLTNSDTHLLQGSLTTLTSPGSSPSVQCSPRGKNIQGG 166  
DB 1 YICEVEDQKEVQLLVGLTNSDTHLLQGSLTTLTSPGSSPSVQCSPRGKNIQGG 60  
QY 167 KTLVSQLELDSDGTWCTVYQONOK 191  
DB 61 RTLSVPOLERQDSGTWCTVNSQDOK 85  
RESULT 20  
QY 077601 PRELIMINARY; PRT; 86 AA.  
AC 077601;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3) (Fragment).  
OS Lophocebus albigena albigena.  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Lophocebus.  
OX NCBI\_TaxID=75568;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98320644; PubMed=9656488;  
RA Harris E.E., Disotell T.R.;  
RT "Nuclear gene trees and the phylogenetic relationships of the mangabey (primates: Papionini)." ;  
RL MoJ. Biol. Evol. 15:892-900(1998).  
CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY SIMILARITY).  
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE AND 1 C2-LIKE DOMAIN.  
DR EMBL; AF057391; AAC25135.1; -.  
DR HSSP; P01730; 1CDY.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR InterPro; IPR007110; Ig-like.  
KM Immunoglobulin domain; T-cell; MHC; Transmembrane.  
FT NON\_TER 1  
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.  
FT CARBOHYD 20 >86 IG-LIKE C2-TYPE DOMAIN.  
FT DISULFD 49 78 BY SIMILARITY.  
FT NON\_TER 86 86  
SQ SEQUENCE 86 AA; 9463 MW; 2BD97A88464FBAB CRC64;  
Query Match 29.5%; Score 388; DB 6; Length 86;  
Best Local Similarity 87.1%; Pred. No. 2.1e-26;  
Matches 74; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 107 YICEVEDQKEVQLLVGLTNSDTHLLQGSLTTLTSPGSSPSVQCSPRGKNIQGG 166  
DB 1 YICEVEDQKEVQLLVGLTNSDTHLLQGSLTTLTSPGSSPSVQCSPRGKNIQGG 60  
QY 167 KTLVSQLELDSDGTWCTVYQONOK 191  
DB 61 RTLSVPOLERQDSGTWCTVNSQDOK 85  
RESULT 21  
QY 077600 PRELIMINARY; PRT; 86 AA.  
AC 077600;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3) (Fragment).  
OS Lophocebus albigena albigena.  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Lophocebus.  
OX NCBI\_TaxID=75568;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98320644; PubMed=9656488;  
RA Harris E.E., Disotell T.R.;  
RT "Nuclear gene trees and the phylogenetic relationships of the mangabey (primates: Papionini)." ;  
RL MoJ. Biol. Evol. 15:892-900(1998).  
CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY SIMILARITY).  
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE AND 1 C2-LIKE DOMAIN.  
DR EMBL; AF057391; AAC25135.1; -.  
DR HSSP; P01730; 1CDY.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR InterPro; IPR007110; Ig-like.  
KM Immunoglobulin domain; T-cell; MHC; Transmembrane.  
FT NON\_TER 1  
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.  
FT CARBOHYD 20 >86 IG-LIKE C2-TYPE DOMAIN.  
FT DISULFD 49 78 BY SIMILARITY.  
FT NON\_TER 86 86  
SQ SEQUENCE 86 AA; 9463 MW; 2BD97A88464FBAB CRC64;  
Query Match 29.5%; Score 388; DB 6; Length 86;  
Best Local Similarity 87.1%; Pred. No. 2.1e-26;  
Matches 74; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

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AC 077600;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)
DE (Fragment).
OS Lophocobus aeterinus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Lophocobus.
OC NCBI_TaxID=75566;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; PubMed=9656488;
RA Harris E.E., Disotell T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the
RT mangabeys (primates: Papionini).";
RL Mol. Biol. Evol. 15:892-900(1998).
CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC SIMILARITY).
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR EMBL, AF057390; AAC25134.1; -.
DR HSSP, P01730; ICDY.
DR GO, GO:0016021; C:Integral to membrane; IEA.
DR InterPro, IPR007110; Ig-like.
KM Immunoglobulin domain; Glycoprotein; T-cell; MHC; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 19 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 49 78 BY SIMILARITY.
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9476 MW; A9D97A88464F83BE CRC64;

Query Match 29.1%; Score 383; DB 6; Length 86;
Best Local Similarity 85.9%; Pred. No. 5,7e-26;
Matches 73; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 107 YICEVEDEKQEVLLVGLTANSPDTHLLOGOSLTLTLESPGSSPSVQCRSPKKNIOG 166
DB 1 YICEVEDEKQEVLLVGLTANSPDTHLLOGOSLTLTLESPGSSPSVQCRSPKKNIOG 60
QY 167 KTLVSQGLQDSGCTWTCTYLQNK 191
DB 61 RTLSVPLERODSGTCTWTCTVNSQDOK 85

RESULT 22
Q13969 PRELIMINARY; PRT; 71 AA.
AC Q13969;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD4 protein (Fragment).
DE CD4.
GN CD4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Zverev V.V., Blinov V.M., Nedospasov S.A.;
RT "Splice-mediated insertion of antisense and sense Alu repeats in human
RT CD4 gene: identification of three exons of CD4 mRNA.";
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RN 12;
RP SEQUENCE FROM N.A.
RX MEDLINE=95407135; PubMed=7676667;

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RA Zverev V.V., Sidorov A.V., Nedospasov S.A., Malushova V.V.,
RA Udajova I.A., Andzhaparidze O.G., Blinov V.M.;
RT "Nucleotide sequence of two exons of the human T-lymphocyte CD4
RT receptor gene.";
RL Vopr. Virusol. 40:100-102(1995).
DR EMBL, X87579; CAA60883.1; -.
DR EMBL, S79267; AAB35273.1; -.
DR PIR, I60082; I60082.
DR HSSP, P01730; ICDY.
DR GO, GO:0004872; F:receptor activity; IEA.
DR InterPro, IPR007110; Ig-like.
DR PROSITE, PS50835; IG_LIKE; 1.
KM Receptor.
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 7844 MW; A5C9D84816135C86 CRC64;

Query Match 27.1%; Score 357; DB 4; Length 71;
Best Local Similarity 98.6%; Pred. No. 8,3e-24;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVFRLVLVQLALPAPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNQIK 60
DB 1 MNRGVFRLVLVQLALPAPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNQIK 60
QY 61 ILGNQGSFLTK 71
DB 61 ILGNQGSFLTK 71

RESULT 23
Q29027 PRELIMINARY; PRT; 99 AA.
AC Q29027;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD4, allele 1 (Fragment).
DE CD4, allele 1 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sui.
OC NCBI_TaxID=9823;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=H183; TISSUE=Blood;
RX MEDLINE=93329116; PubMed=8335933;
RA Gustafsson K., Germania S., Sundt T.M., Sachs D.H., Leguenn C.;
RT "Extensive allelic polymorphism in an exposed region of the
RT minature. . . .";
RL J. Immunol. 151:1365-1370(1993).
DR EMBL, X65629; CAA46583.1; -.
DR PIR, I47131; S21461.
DR HSSP, P01730; ICDY.
DR InterPro, IPR007110; Ig-like.
DR InterPro, IPR003596; Ig_V.
DR Pfam, PF00047; Ig_1.
DR SMART, SM00406; IGV_1.
DR PROSITE, PS50835; IG_LIKE; 1.
FT NON_TER 99 99
SQ SEQUENCE 99 AA; 11170 MW; 40BF080699CF5DOC CRC64;

Query Match 23.2%; Score 305.5; DB 6; Length 99;
Best Local Similarity 60.2%; Pred. No. 4e-19;
Matches 59; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 32 KKGDVVELTCTASQKKSIOFHMKNSNQIKILGNQGSFL-TKGPSKLNDRADRSRLWDG 90
DB 1 KAGDLALPCHSSQKKNLPFNKNSNQIKILGSGHGFMTASVTELTSLRDSKKNMWDHG 60
QY 91 NPLLIKNLKIENSDTYICEVEDEKQEVLLVGLTAN 128
DB 61 SFLIINKLEVTDGIVICEVEDKRIEVLVRLTAS 98

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RESULT 24
Q29028      PRELIMINARY;      PRT;      99 AA.
ID Q29028;
AC Q29028;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CD4, allele 2 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN#1183; TISSUE=Blood;
RA MEDLINE=93329116; PubMed=8335933;
RA Guetartson K., Germana S., Sundt T.M., Sachs D.H., Leguern C.;
RT "Extensive allelic polymorphism in an exposed region of the
RT Malariae. . . . .";
RL J. Immunol. 151:1365-1370(1993).
DR EMBL; X65630; CAA46584.1; -.
DR PIR; I47132; S21462.
DR HSSP; P01730; ICDY.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1
FT NON TER 99
SQ SEQUENCE 99 AA; 11390 MW; C22955EA28318F CRC64;

Query Match 21.3%; Score 280.5; DB 6; Length 99;
Best Local Similarity 56.1%; Pred. No. 6.2e-17;
Matches 55; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

QY 32 KKGDVLTCTASQKSIQFHWKNSNOIKILGNQSFITKCP-SKUNDRADRSRLMDQG 90
DB 1 KAGGLAEIPCHSSQKQKLPFSWKNSDQIKIRSHRNLMHKASVTELSRLDSKKNMMDHG 60

QY 91 NFPLIINKLIKEDSDTYICEVEDQKEEYQLVPGITAN 128
DB 61 GFPLIKLEVTDSGYICEVEDKRIEYQLVPLRLTAS 98

RESULT 25
Q290B5      PRELIMINARY;      PRT;      482 AA.
ID Q290B5;
AC Q290B5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 precursor.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Anseriformes; Anatidae; Anas.
OX NCBI_Taxid=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Chan S.W.S., Middleton D.L., Lundqvist M., Marr G.W., Higgins D.A.;
RA Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF318701; AAK59279.1; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR Pfam; PF00047; IG_4.
DR SMART; SM00409; IG_3.
DR PROSITE; PS50835; IG LIKE; 2.
KW Signal.
FT SIGNAL 1
SQ SEQUENCE 482 AA; 54624 MW; BDA08E8C6172AD0B CRC64;

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Query Match 13.1%; Score 172; DB 13; Length 482;
Best Local Similarity 25.7%; Pred. No. 1.5e-06;
Matches 57; Conservative 41; Mismatches 76; Indels 48; Gaps 9;

QY 8 RHLLVQLALLPAAQGNKVLGKGDVLTCTASQKSIQFHWK-----NSNQIK 60
DB 12 RAVFVLQLGLG--THIMAHQOQIVGEGEVILNC---KKHKQVTKVEYDAGSSAIIIQ 66

QY 61 ILGNQSFITKCP-SKUNDRADRSRLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEYQL 120
DB 67 ILACK---IFKGRAPMSDRSET-----NQNKHLKVSNLRIISDAGTYICEGSDRNISL 118

QY 121 LVFGLTANSPDTHILQSGSLTIT-LESPGSSPS-----VQCSPPCKN 162
DB 119 HVVLTITSSNGYFLPGDDELITVHKSPKSPRSTITFLNSHNRVTPVQLNETPQ--- 175

QY 163 IGGKTLISVQLKQSDSGTWTCTVLQN---QKKVEKIDIV 200
DB 176 ---KYALKVKQLQPTDSGTWICNNHSDSPSINENISFVVKVL 214

RESULT 26
Q29123      PRELIMINARY;      PRT;      538 AA.
ID Q29123;
AC Q29123;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Vascular cell adhesion molecule.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA MEDLINE=94271236; PubMed=7516159;
RA Tsang Y.T., Haskard D.O., Robinson M.K.;
RT "Cloning and expression kinetics of porcine vascular cell adhesion
RT molecule. . . . .";
RL Biochem. Biophys. Res. Commun. 201:805-812(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=96106491; PubMed=8525525;
RA Mueller J.P., Evans M.J., Coffell R., Rother R.P., Matlis L.A.,
RA Elliott E.A.;
RT "Porcine vascular cell adhesion molecule (VCAM) mediates endothelial
RT cell adhesion to human T cells. Development of blocking antibodies
RT specific for porcine VCAM. . . . .";
RL Transplantation 60:1299-1306(1995).
DR EMBL; L43124; AAB59281.1; -.
DR HSSP; P19320; IVCAM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro: IPR003987; ICM_VCAM-1.
DR InterPro: IPR003598; IG-like.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003989; VCAM-1.
DR Pfam; PF00047; IG_5.
DR PRINTS; PR01472; ICMVCAM1.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00408; ICG2; 3.
DR PROSITE; PS50835; IG LIKE; 4.
KW Immunoglobulin domain.
SQ SEQUENCE 538 AA; 58713 MW; 8A7CD36D0A2F0717 CRC64;

Query Match 12.0%; Score 157.5; DB 6; Length 538;
Best Local Similarity 25.0%; Pred. No. 3.2e-05;
Matches 50; Conservative 38; Mismatches 71; Indels 41; Gaps 6;

QY 32 KKGDVLTCTASQKSIQFHWKNSNOIKILGNQSFITKCP-SKUNDRADRSRLMDQGN 91

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Db      235 QEDGSVMWMTCTSGRLAPQISW-----SKKLDNGQQLL-----SGN 271
Qy      92 FPLIINKLKIEDSDTYICE---VEDQKEVQLLV-----FGLTANSDTHLLQGQSLTL 141
Db      272 ATLTLTAMRMEDSGIYCEGVNPGVTRNRKEVELTVQAPRDTTISVNPSTLEBGSVNM 331
Qy      142 TLESPPGSSPSV---QCRSPRGKNIQGGKTLVSQLELQDSGTWCTVLQ---NOKKY 193
Db      332 TCSSDGPAPKILMSKRLRGNIPELSENTTLTLTSTKMEDSGIYVCDGINQGINRKEY 391
Qy      194 EFKIDIVPRASALPAPPTGS 213
Db      392 ELIIQAAPKDLQTLAPFSES 411

RESULT 27
ID Q28939 PRELIMINARY; PRT; 538 AA.
AC Q28939;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE Vascular cell adhesion molecule precursor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=94271236; PubMed=7516159;
RA Trang Y.T., Haekard D.O., Robinson M.K.;
RT "Cloning and expression kinetics of porcine vascular cell adhesion
molecule."
RL Biochem. Biophys. Res. Commun. 201;805-812(1994).
DR EMBL; U08351; AAA21542.1; -.
DR PIR; JC2457; JC2457.
DR HSP; P19320; 1YCA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003987; ICAM VCAM-1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG C2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; IG_5.
DR PRINTS; PRO1472; ICAMVCAM1.
DR SMART; SMO0408; IGc2_3.
DR PROSITE; PS50835; IG LIKE; 4.
KM Immunoglobulin domain; Signal.
FT SIGNAL 1 24
FT CHAIN 25 538 VASCULAR CELL ADHESION MOLECULE.
SQ SEQUENCE 538 AA; 58795 MW; EC29D11B224F7261 CRC64;

Query Match 11.9%; Score 156.5; DB 6; Length 538;
Best Local Similarity 24.5%; Pred. No. 3.9e-05;
Matches 49; Conservative 39; Mismatches 71; Indels 41; Gaps 6;

Qy      32 KKGDYVELCTASQKSIQFHWKNSNQIKLQNGSFLTKGPSKLNDRADRSRLMDQGN 91
Db      235 QEDGSVMWMTCTSGRLAPQISW-----SKKLDNGQQLL-----SGN 271
Qy      92 FPLIINKLKIEDSDTYICE---VEDQKEVQLLV-----FGLTANSDTHLLQGQSLTL 141
Db      272 ATLTLTAMRMEDSGIYCEGVNPGVTRNRKEVELTVQAPRDTTISVNPSTLEBGSVNM 331
Qy      142 TLESPPGSSPSV---QCRSPRGKNIQGGKTLVSQLELQDSGTWCTVLQ---NOKKY 193
Db      332 TCSSDGPAPKILMSKRLRGNIPELSENTTLTLTSTKMEDSGIYVCDGINQGINRKEY 391
Qy      194 EFKIDIVPRASALPAPPTGS 213

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Db      392 ELIIQAAPKDLQTLAPFSES 411

RESULT 28
ID Q96V7 PRELIMINARY; PRT; 487 AA.
AC Q96V7;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE CD4 protein precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H.B2; TISSUE=Thymus;
RX MEDLINE=99218434; PubMed=10201936;
RA Koskinen R., Lammimaki U., Tregaskes C.A., Salomonsen J., Young J.R.,
Vainio O.;
RT "Cloning and modeling of the first nonmammalian CD4."
RL J. Immunol. 162;4115-4121(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B12;
RA Koskinen R.H., Salomonsen J., Tregaskes C.A., Young J.R.,
Goodchild M., Bumstead N., Vainio O.;
RT "The chicken CD4 gene has remained conserved in evolution."
RL Immunogenetics 0:0-0(2002).
DR EMBL; Y12012; CAA72740.1; -.
DR EMBL; A0401223; CAC82027.1; -.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_3.
DR PROSITE; PS50835; IG LIKE; 2.
KM Signal.
FT SIGNAL 1 28
FT CHAIN 25 487 VASCULAR CELL ADHESION MOLECULE.
SQ SEQUENCE 487 AA; 54985 MW; B9CBA92EC9F7F45B CRC64;

Query Match 11.6%; Score 153; DB 13; Length 487;
Best Local Similarity 27.8%; Pred. No. 6.9e-05;
Matches 59; Conservative 28; Mismatches 87; Indels 38; Gaps 8;

Qy      10 LLLVQLALLPAATQGNKVLGKKEPTVELTCTA-SQKSIQFHWKNSNQIKLQNGSFLTKGPSKLNDRADRSRLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQLLV 63
Db      14 VILVQLGLTPITMAQEQOI-GIAGEVILSKAINNQDGTCTWTKYKVESSTIISFS 72
Qy      64 NGGSFLTKGPSKLNDRADRSRLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQLLV 123
Db      73 KQVFKGKAPM-----THRELSNNSKKLVSDLSDDAGITCACSPPVVISLHP 125
Qy      124 GLTANSDTHLLQGQSLTLT-ESPSSPS-----VOCSPRGKNIQ 165
Db      126 KLITSSNGHFLTMEDELTLTMONSSHQPHLSIKLFNINNDIYTTELDEARQ-KYI-- 182
Qy      166 GKTLVSQLELQDSGTWCTVLQNGKVEFKI 197
Db      183 ---LKLKQKALDSDGTWCHVYNSPSINQNI 211

RESULT 29
ID Q9D7B8 PRELIMINARY; PRT; 287 AA.
AC Q9D7B8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE 2310016B05RIK protein.
GN DIERTD736E OR 2310016B05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
RA Akawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kaakawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Macsuo Y., Nikaido I., Peeble G., Quackenbush J.,
RA Schriml L.M., Strubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gutwirth S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlschki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009375; BAB26251.1;
DR MGI; MGI:1289168; D11Etd736e.
DR InterPro; IPR003599; 1g_1.
DR InterPro; IPR007110; 1g_1like.
DR Pfam; PF00047; 1g_1.
DR SMART; SM00409; 1g_1.
DR PROSITE; PS50835; 1g_LIKE; 1.
SQ SEQUENCE 287 AA; 32061 MW; D9324D3308A03639 CRC64;

Query Match 10.9%; Score 144; DB 11; Length 287;
Best Local Similarity 23.0%; Pred. No. 0.00021;
Matches 68; Conservative 46; Mismatches 110; Indels 72; Gaps 11;

QY 8 RHLLVQLALPPA--ATGKNNVVGKKGDTVELTCTASQK-KSIQFWKNSNOIK--- 60
DB 2 RPLVLMGCLVLPGEALKPKKISGFEQDTVSLCTVEVKKKRYKRCQGILVSRG 61
QY 61 ---ILGNGSFLTGKPSKLNDRASRLMDQGNFLLIKLKIEDSDTYICEV---D 113
DB 62 GDIVYANDQGVTRKMSIR---DSPQEL---SFTVMRLTLTKDSKTYCGIDRLGRD 114
QY 114 QKEEYQVLV-----GLTNSDTHLQSGSLTLTSPGSSPSVQCRSP---R 159
DB 115 ESFEVTLVFPQSYRPPVWMLPTTPQDS-----RAVASVSKPSVSTPMVMMAFVLIL 169
QY 160 GKNIQGGKTLVSQLELQDSGTWTCTVQLQNGKVEFK-----IDIVPRA 203
DB 170 SLILAAGIATGSHMLRWKMKAMLATETQKNEKYLFTSLPGNGWTTEDSTIDLAVPEEC 229
QY 204 -----SLTPAPPT---GSALPDPOTASALPD-----PPAASLTPAALAVISFL 243
DB 230 LRNIINPSAVPSPETQNSQSTEEBAARSLLDDKEDVMAPPLOMSAEELAFSEPT 285

RESULT 30
Q9GKR2 PRELIMINARY; PRT; 650 AA.
AC Q9GKR2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Vascular cell adhesion molecule-1 6D variant lacking D7 precursor.
GN VCAM1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Muscle;
RA Muroya S., Nakajima I., Chikuni K.;
RT "Novel alternative splicing variant of bovine vascular cell adhesion molecule-1."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB052747; BAB19782.1; -
DR HSSP; P19320; 1VCA.
DR InterPro; IPR007110; 1g_1like.
DR InterPro; IPR003598; 1g_c2.
DR Pfam; PF00047; 1g_6.
DR SMART; SM00408; 1g_c2; 2.
DR PROSITE; PS50835; 1g_LIKE; 4.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 24
FT CHAIN 25 650
FT VASCULAR CELL ADHESION MOLECULE-1 6D
FT VARIANT LACKING D7.
SQ SEQUENCE 650 AA; 71821 MW; 24244573EF2B5E40 CRC64;

Query Match 10.7%; Score 141; DB 6; Length 650;
Best Local Similarity 25.6%; Pred. No. 0.0011;
Matches 52; Conservative 35; Mismatches 60; Indels 56; Gaps 10;

QY 32 KKQDTVELTCTASQKSIQFWKNSNOIKLGNQGSFLTGKPSKLNDRASRLMDQGN 91
DB 238 QEGDSVTMTCSAGLPAPRLIMS-----KKL-----DNGN 267
QY 92 FPLIKK-----LKIEDSDTYICE---VEDQKEVQLV-----FGLTNSDTHLQ- 135
DB 268 RQLSENATLTLIMRADSGIYVCEGNPVGKRYKRYLTVQKNFTVEISPPQIAAQ 327
QY 136 -GQSLTLTLESPPSSPSVQCR---SPRGKNI--QSGK-TLSVSOLELQDSGTWTCTVL 187
DB 328 VGDSIVLTCVDRDCESPSFWRILIDSPLNQVASESKSTLTLSPVSEHFHYLCTVM 387
QY 188 QNGKVEFKIDIVPRASALPAP 210
DB 388 CGQKLEKRIQVKE--YSPSPNP 408

RESULT 31
Q9GKR3 PRELIMINARY; PRT; 739 AA.
AC Q9GKR3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Vascular cell adhesion molecule-1 7D variant precursor.
GN VCAM1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Muscle;
RA Muroya S., Nakajima I., Chikuni K.;
RT "Novel alternative splicing variant of bovine vascular cell adhesion molecule-1."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB052746; BAB19650.1; -
DR HSSP; P19320; 1VCA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003987; 1CAM_VCAM-1.
DR InterPro; IPR007110; 1g_1like.
DR InterPro; IPR003598; 1g_c2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; 1g_7.

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Db		237	ECCGSSVTWTCASBEGIPPEQPIFWMSKRLDNGML--L--	
Qy		89	OQNPFLLIKNLIKIEDSPDYIC-----EVEDDQKEEVQLVY----FGLTANSDTHLLQ--GQS 138	
Db		271	SGNALTLITLAMRLEDSCGYVEGWEGNEGKCKOGEKVELLVQEKFPVELISPPQQIIAQIGDS 330	
Qy		139	LTLTLESPPGSSPS---VQCRRSFRG--KNIIQGK-TLSVSQLELDQSGTWCTVLONOK 191	
Db		331	VVLITGVGTDCESPFSFWRQTQIDSLPGSTVKVEGAKSFTLTLSPVALEMHSYLCTVTCGHK 390	
Qy		192	KYE--FKIDI 199	
Db		391	KLEKGIRKVDL 400	
 RESULT 33				
ID	092626	PRELIMINARY:	PRT: 1496 AA.	
AC	092626;			
DT	01-FEB-1997 (TrEMBLrel. 02,			
DT	01-FEB-1997 (TrEMBLrel. 02,			
DT	01-OCT-2003 (TrEMBLrel. 25,			
DT	MYELOBLAST KIAA0230 (Fragment).			
GN	KIAA0230.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=97191544; PubMed=9039502;			
RA	Nagae T., Seki N., Ishikawa K., Ohira M., Kawarabayashi Y., Ohara O.,			
RA	Tanaka A., Kotani H., Miyajima N., Nomura N.;			
RT	"Prediction of the coding sequences of unidentified human genes. VI.			
RT	The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by			
RL	analysis of cDNA clones from cell line KG-1 and brain."			
RNA	DNA Res. 3:321-329(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Melanoma;			
RX	MEDLINE=95048383; PubMed=7959781;			
RA	Weiler S.R., Taylor S.M., Deans R.J., Kan-Mitchell J., Mitchell M.S.,			
RT	Trent J.M.;			
RT	"Assignment of a human melanoma associated gene MG50 (D2S448) to			
RL	chromosome 2p25.3 by fluorescence in situ hybridization.";			
RL	Genomics 22:243-244(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Melanoma;			
RC	Mitchell M.S., Kan-Mitchell J., Minev B., Edman C., Deans R.J.;			
RT	"Identification of a novel melanoma gene (MG50) - likely the gene for			
RT	IL-1 receptor antagonist - which encodes epitopes recognized by human			
RT	cytolytic T lymphocytes.";			
RL	Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; D86983; BAA13219.1; -.			
DR	EMBL; AF200348; AAP06354.1; -.			
DR	HSSP; P05164; ICPY			
DR	GO; GO:0005152; Finterleukin-1 receptor antagonist activity; NAS.			
DR	GO; GO:0006955; Pimmune response; NAS.			
DR	InterPro; IPRO02007; AnIm_peroxidase.			
DR	InterPro; IPRO07110; IG-like.			
DR	InterPro; IPRO03598; IG_c2.			
DR	InterPro; IPRO01611; LRR			
DR	InterPro; IPRO00463; LRR_Cterm.			
DR	InterPro; IPRO00372; LRR_Nterm.			
DR	InterPro; IPRO03591; LRR_typ.			
DR	InterPro; IPRO02016; Peroxidase.			
DR	InterPro; IPRO01007; VWF_C.			
DR	Pfam; PF03098; An_peroxidase; 1.			
DR	Pfam; PF00047; Ig_4.			
DR	Pfam; PF00560; LRR; 5.			
DR	Pfam; PF01463; LRRT; 1.			

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DR Pfam; PF00093; vwc; 1.
DR PRINTS; PRO0457; ANPEROXIDASE.
DR SMART; SM00408; IGC2; 4.
DR SMART; SM00082; LRCT; 1.
DR SMART; SM00013; LRNT; 1.
DR SMART; SM00369; LRR_TYP; 4.
DR SMART; SM00214; vwc; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS50292; PEROXIDASE_3; 1.
DR PROSITE; PS01208; vwc_1; 1.
DR PROSITE; PS50184; vwc_2; 1.
DR Immunoglobulin domain.
FT NON TER 1
SQ SEQUENCE 1496 AA; 167209 MW; E9B9A7069BFBABF CRC64;

Query Match 10.0%; Score 131.5; DB 4; Length 1496;
Best Local Similarity 26.5%; Pred. No. 0.023;
Matches 60; Conservative 27; Mismatches 92; Indels 47; Gaps 9;

Oy 34 GDTVELTCTASQKKSIOFHMKNSNQIKILNGSGFLTKGPSKLNDRADRSRLMDQGNFP 93
Db 277 GNTVYFTCTRAGNPKPEIILRN-----NELSKTDSRLNLDDGT-- 318
Oy 94 LIINKLKIEDSDTYICEV-----EDQKEVDLVFGLTAN-----SDTHLLOGSILTL 141
Db 319 LMIGNTQRTDGIQCMANKVAGEVKIQEVLTRYGFAPRTFVIQPNTEVLVGESVTL 378
Oy 142 -----TLSPSSSSSVQCRRP---RGKNIQGGKTLVSQLELSDSGTWTCVTIYONKV 193
Db 379 ECSATGHPPIPISWTRGDRPLPVDPRVNIIPSGGLYIQNVQSGSGHYACSATNIDSV 438
Oy 194 EFKDIVPRASALP---APPGSALPDQGT---ASALPDPPASAS 232
Db 439 HATAPFI--VQALPQFTVTPDQVIVIEGQIVDFQCEAKGNPPVIA 482

RESULT 34
O8NPP4 PRELIMINARY; PRT; 955 AA.
AC O8NPP4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glycoyl-phosphatidyl-inositol-MAM.
GN GPM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22077705; Pubmed=12082541;
RA De Juan C., Infesta P., Gonzalez-Quevedo R., Moran A.,
RA Sanchez-Pernate A., Torres A.J., Balbrea J.L., Diaz-Rubio E.,
RA Cances J., Benito M.;
RT "Genomic organization of a novel glycosylphosphatidylinositol MAM gene
RT expressed in human tissues and tumors.";
RL Oncogene 21:3089-3094(2002).
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL; AF478693; AA077220.1; -.
DR Genew; HGNC:19267; MDGA1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016163; F:nitrogenase activity; IEA.
DR GO; GO:0003939; P:nitrogen fixation; IEA.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003599; IG_1-like.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000998; MAM_domain.
DR InterPro; IPR000318; Nitrogene_comp1.
DR Pfam; PF00047; IG; 6.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PRO0020; MAMDOMAIN.

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DR SMART; SM00409; IG; 6.
DR SMART; SM00408; IGC2; 6.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS50060; MAM_2; 1.
DR PROSITE; PS00699; NITROGENASE_1; 1.
DR Glycoprotein; Immunoglobulin domain.
SQ SEQUENCE 955 AA; 105790 MW; BD41A1EB10A05962 CRC64;

Query Match 9.9%; Score 130; DB 4; Length 955;
Best Local Similarity 23.2%; Pred. No. 0.0044;
Matches 57; Conservative 40; Mismatches 91; Indels 58; Gaps 11;

Oy 10 LLLVQLALLPAA-----TQGNKVILGKGDVVELTCTASQKKSIOFHMKNSNQIKI 61
Db 14 LVLLRLCLLPPTGIPVPSVDFNRTGNTIVRQSGTALIRCVEDKNS-KVAMILNRSGIIF 72
Oy 62 LKNGSGFLTKGPSKLNDR--DSRRSLMDQGNPFLIINKLKIEDSDTYICEVEQKE--- 116
Db 73 AGHD-----KMSLDRAVELEKRHSI---EYSLRIQKVDVDEGSYTSVQTHPEPT 121
Oy 117 -EVQLAVFG---LTANSPTHLLOGSILTLSPSSSSSVQCR--SPRGKNIQGGKT- 168
Db 122 SQVTLIVQVPPKSNISSDVTYVNGSVNTLVCMANGRPPEVITWRHLTPGREGESEY 181
Oy 169 LSVQLELQDSGTWTCVTIQ-----NOKVVEFKDIVP-----RA 203
Db 182 LEIIGITREOSGKVECAANEVSSADVQKVTNVNPPFTITESKSNATTTGRQASLCKEA 241

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RESULT 35
O8IV49 PRELIMINARY; PRT; 338 AA.
AC O8IV49;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to limbic system-associated membrane protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strauberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033803; AA033803.1; -.
DR InterPro; IPR003599; IG_1-like.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 338 AA; 37393 MW; 88CF00E07302817B CRC64;

Query Match 9.9%; Score 130; DB 4; Length 338;
Best Local Similarity 23.2%; Pred. No. 0.0044;
Matches 57; Conservative 40; Mismatches 91; Indels 58; Gaps 11;

Oy 36 TVELTCTASQKKSIOFHMKNSNQIKILNGSGFLTKGPSKLNDRADRSRLMDQGNPFI 95
Db 152 TVFLRCTVNSNPPARFTWKQSD-----TLHSQDNG-VDIYEPLYTGERTKVL 199
Oy 96 -IKNLKIEDSDTYICEVEDQKE---EVQLAVFGLTANSPTHLLOGSILTLSPSSSP 151
Db 200 KLKMLRQDQVASYTCQSVANVCGIPDKATIFRLTNTTAPALK-LSVNETLVNPGENV 258
Oy 152 SVQC-----RSPRGKNIQGGKTLVSQLELSDSGTWTCVTIYON 189
Db 259 TVQCLTNGDPLPOLQWSHGPGPLGLAAGG-TLSIPSVQARDSGYNTCTATNN 313

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QY 204 SALPAP 209  
DB 242 SAVPAP 247

## RESULT 36

Q9QY38 PRELIMINARY; PRT; 1259 AA.

AC Q9QY38; 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Neural cell adhesion molecule 11.  
GN L1CAM.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

RE SEQUENCE FROM N.A.  
RA Platzner M., Brenner V., Reichwald K., Wiene T., Oksche A.,  
RA Rosenthal A.;  
RT "Comparative sequence analysis of the mouse L1cam locus and the  
RT corresponding region of human XG28.";  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF133093; AAF22153.1; -.  
DR HSSP; P20241; ICFB.  
DR MGI; MGI:96721; L1cam.  
DR GO; GO:0007411; P:axon guidance; IMP.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003598; IG\_c2.  
DR Pfam; PF00047; IG; 6.  
DR Pfam; PF00047; IG; 4.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00408; IGC2; 5.  
DR PROSITE; PSS0835; IG\_LIKE; 6.  
KW Immunoglobulin domain.  
SQ SEQUENCE 1259 AA; 140916 MW; 25743C039892A22F CRC64;

Query Match 9.8%; Score 130; DB 11; Length 1259;  
Best Local Similarity 23.9%; Pred. No. 0.005;  
Matches 56; Conservative 32; Mismatches 96; Indels 50; Gaps 9;

QY 10 LLLVQLALPPATQGNKVVLGKKGDVVELTCTASQKKSIO--FHWKNSQIKILGNQGS 67  
DB 507 ILANLQVKEATQITQGPRAIEKKGAVTFQCASFPDSIQASTWMDGR----- 557  
QY 68 FLTKGSPKLNDRADRSRLSDQGNFPLIKLKIKIEDSDTYIC---EVEDQKEVOLVLF 123  
DB 558 -----DLQERGSDDYFLIEDGK--LVISLDYSDGNSCVASTELDEVESRAQLLV 608  
QY 124 GLTAN-----SDPHLQGSLLTTLSPSSPSVQCRSP-----RGKNIQGGKTL 169  
DB 609 GSPEPVHLELSDHLLKQSGVHLSSW-----SPAEDHNSPIEKYDIEFEDKEAPAKMF 662  
QY 170 SVSOLQDSGTWTCTVQLQNKQVE--FKIDIVRASALPAPPTGSALPPQTA 221  
DB 663 SLGKV---PQNGSTLTKLSPVHYTFRTVAINKYGPGEPSFSEVTVPEAA 712

## RESULT 37

Q812P8 PRELIMINARY; PRT; 437 AA.

AC Q812P8; 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Nectin-like protein 3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RE SEQUENCE FROM N.A.  
RA Geringrich J.R., D'Angelo A., Chang G.M., Greenberg N.M.;  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF538973; AAN16368.1; -.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003598; IG\_c2.  
DR Pfam; PF00047; IG; 3.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00409; IGC2; 3.  
DR SMART; SM00408; IGC2; 3.  
DR PROSITE; PSS0835; IG\_LIKE; 3.  
SQ SEQUENCE 437 AA; 47593 MW; D23DB347F5E5F023 CRC64;

Query Match 9.8%; Score 129.5; DB 4; Length 437;  
Best Local Similarity 19.8%; Pred. No. 0.0068;  
Matches 57; Conservative 43; Mismatches 101; Indels 87; Gaps 12;

QY 10 LLLVQLALPPATQGNKVVLGKKGDVVELTCTASQKKSIOFHWKNS 57  
DB 3 VFLCNLSLVPAASKNKVKSGQGPELTQNTVVEGTAIILTCRVQDNDNTSLQWSNPA 62  
QY 58 QIKILGNQGSFLTKGSPKLNDRADRSRLSDQGNFPLIKLKIKIEDSDTYICE---VEDQ 114  
DB 63 Q-----QTLVFDKALADNRILVRA SMHE--LSISVDSVLSDEGGYTCSLFTMPVK 114  
QY 115 KEEVOLVPEGL-----TANSDPHLQGSLLTTLSPSSPSVQCR--SPRGKNIQGGK 168  
DB 115 TSKAVYLTIVGVEPEKPGISGSSPVMEGDLMOQLCKT--SGSKPAADIRFPKDKK 169  
QY 169 LSVSOLQDSGTWTCTVQLQNKQVEFKID----- 198  
DB 170 -DVKYLKKEDANKKRTV--SSTLDFRVDRSDDGVAIVICRVDSLSLNTPTPVAMQVLEI 225  
QY 199 -IVPRASALPAP-----TGSALPDP-----QTASALPDP 227  
DB 226 HYPSVKIITPSTFPQEGPLITCSKGRPLPEVPLWTKDGSELDP 273

## RESULT 38

Q8SP16 PRELIMINARY; PRT; 731 AA.

AC Q8SP16; 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Polymetric immunoglobulin receptor.  
GN PIGR.

OS Macropus eugenii (Tamar wallaby).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
OX NCBI\_TaxID=9315;

RE SEQUENCE FROM N.A.  
RA Taylor C.L., Harrison G.A.;  
RT "cDNA cloning of the polymetric immunoglobulin receptor of the  
RT marsupial Macropus eugenii (tamar wallaby).";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF17205; AAK69593.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_1like.  
DR Pfam; PF00047; IG; 5.  
DR SMART; SM00409; IGC; 5.  
DR PROSITE; PSS0835; IG\_LIKE; 3.  
KW Receptor.  
SQ SEQUENCE 731 AA; 80253 MW; 91BDF3BC347B8C17 CRC64;

Query Match 9.8%; Score 129; DB 6; Length 731;  
Best Local Similarity 23.6%; Pred. No. 0.015;  
Matches 65; Conservative 47; Mismatches 100; Indels 64; Gaps 11;

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QY 2 NRGVPRRLTLVLQALPAPATGKGVKGGDTVELTCTASOK--KSIOFHMKNSNOI 59
D 115 SRGLSFDLTQVGDSDNLP-----DSEVITEVGKTVSINCPKSENNODRFLCKDDKS 170
QY 60 KIL-----GNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKLKIEDSDTYICEV-ED 113
D 171 CVLVIDSQNNVGSIDYT-----BRVRFISGTSKSVFVLIISQFKRQDVCTYICAVGED 223
QY 114 QKEVQLLVFGLTANSPTHL---QGOSLT--TLESPPGSSPSVQCR-----156
D 224 SAPRIQKTVDIRKLDPETELVAEQQGSVTLNCAIGTAEMMPYLCPRIKADMTCDLVIN 283
QY 157 -----SPRGKNI-----OGKTLVSQLELQDSGTWTCTVLONOKVE-----194
D 284 SKGFTNNSHTGRILFTPEPSSFSIMITQVKEDAGLYHCAQENGEPSEKPIQALOLF 343
QY 195 -FKIDIVPRASALPAPPTGSALP-----DPQTASAL 224
D 344 VSEETVVPKSPLVVKGPSGVSVTCHYDPKKNMTL 379
```

## RESULT 39

```
Q8BLK3 PRELIMINARY; PRT; 341 AA.
ID Q8BLK3
AC Q8BLK3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Lmbic system-associated membrane protein precursor.
GN B130007004RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=23354683; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK044845; BAC32117.1;
DR MGD; MGI:2442078; B130007004RIK.
DR InterPro; IPR003599; 1g.
DR InterPro; IPR007110; 1g_1like.
DR InterPro; IPR003598; 1g_c2.
DR Pfam; PF00047; 1g_3.
DR SMART; SM00409; 1g_3.
DR SMART; SM00408; 1gc2; 3.
DR PROSITE; PSS0835; 1G LIKE; 3.
SQ SEQUENCE 341 AA; 38086 MW; 949CE792C67E25C3 CRC64;
```

Query Match 9.6%; Score 126; DB 11; Length 341;

Best Local Similarity 22.8%; Pred. No. 0.0099; Indels 58; Gaps 11;

Matches 56; Conservative 41; Mismatches 91;

```
QY 10 LLLVQLALPAA-----TOGNKVLGKKGDVETCTASOKKSIOFHMKNSNOIKI 61
D 14 LVLRLCLLPPTGSPVSVDFNRGTDNITVAGSDTALIRCYVEDKNS-KVAMNLRSGIIF 72
QY 62 LGNQGSLTKGSPSKLNDRA--DSRRSLMDQGNPFLIKLKIEDSDTYICEVEDQCR--116
D 73 AGHD-----KMSLDPEVLEKRNAL---EYSLRIQKVYVDEGSYTCVSQTOHEPKT 121
QY 117 -EVLTLVFG-----LTANSPTHLQGSITLTLESPPGSSPSVQCR--SPRGKNIQSGKT-168
D 122 SQTLLIVQVPPKINISDVTNNGSVNLTVCANNGRPEPVTWRHLPLGREFEGEEY 181
QY 169 LSVQLELQDSGTWTCTVLQ-----NOKVPEFKIDIVP-----RA 203
```

```
D 182 LEILGTREOSGKYCKRANEVSSADYKQVTVNVPPTTESKSEATTGQASLCKEA 241
QY 204 SALPAP 209
D 242 SAVPAP 247
```

## RESULT 40

```
Q13857 PRELIMINARY; PRT; 226 AA.
ID Q13857
AC Q13857;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Biliary glycoprotein (Fragment).
GN BGP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89139550; PubMed=2537311;
RA Barnett T.R., Drake L., Pickle W. II.;
RA Barnett T.R., Kreischer A., Austen D.A., Goebel S.J., Hart J.T.,
RA Elting J.J., Kamarck M.E.;
RT "Carinoembryonic antigens: alternative splicing accounts for the
RT multiple mRNAs that code for novel members of the carinoembryonic
RT antigen family."
RL J. Cell Biol. 108:267-276(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=93140765; PubMed=8423792;
RA Barnett T.R., Drake L., Pickle W. II.;
RT "Human biliary glycoprotein gene: characterization of a family of
RT novel alternatively spliced RNAs and their expressed proteins."
RL Mol. Cell. Biol. 13:1273-1282(1993).
DR EMBL; M76741; AA57141.1;
DR GO; GO:0005624; C:membrane fraction; TAS.
DR CO; CO:0007565; P:pregnancy; TAS.
DR InterPro; IPR007110; 1g_1like.
DR InterPro; IPR003598; 1g_c2.
DR Pfam; PF00047; 1g_1.
DR SMART; SM00408; 1gc2; 1.
DR PROSITE; PSS0835; 1G LIKE; 1.
KM Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 226 AA; 24045 MW; 8E11929059866970 CRC64;
```

Query Match 9.5%; Score 125.5; DB 4; Length 226;

Best Local Similarity 24.7%; Pred. No. 0.0064; Indels 69; Gaps 13;

Matches 63; Conservative 37; Mismatches 86;

```
QY 11 LVLVQLALPAAQ-----GNKRVLGKKGDVETCTASOKK-SIOFHMKNSNOIKILNQG 66
D 24 IIVTELSPVVAKQIKASKTTVTGDK-DSVNLCTSDTNDTGISIRWFKQNSL-----74
QY 67 SFLTKGSKLNDRADSRSLMDQGNPFLIKLKIEDSDTYICEV-----EDQKEVQL-120
D 75 -----PS-----SERMKLSQGNLTLSINPYKREDAGYWEVFENPISKNSDPTMLN 121
QY 121 -LVFGLTANSPTHLQGSITLTLESPPGSSPSVQCRSPRGKNIQSGKTLVSQLELQDS 179
D 122 EMAF-----HHVAKAGIKLSSNSPASTOSAKITRQNI-----TMLPRLDS 165
QY 180 GTWCTVLONQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPAPASALPALAV 239
D 166 NSMAQAAIL-----PSVSG-SAITONALPQENGLS-----PGAIAGI--VIGV 205
QY 240 ISFLGLGLGVACVL 254
D 206 VALVALIIVALACFL 220
```

```
RESULT 41
Q80U60      PRELIMINARY;      PRT;      1431 AA.
ID Q80U60;
AC Q80U60;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MKIAA0230 protein (Fragment).
GN MKIAA0230.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10099;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries."
RL DNA Res. 10:35-48(2003).
DR EMBL: AK122223; BAC65505.1;
DR GO: GO:0004601; F:peroxidase activity; IEA.
DR GO: GO:0006979; P:response to oxidative stress; IEA.
DR InterPro: IPR002007; Anim_peroxidase.
DR InterPro: IPR003599; IG_1-like.
DR InterPro: IPR007110; IG_2-like.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR003596; IG_v.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR007092; LRR_SDS22.
DR InterPro: IPR003591; LRR_Typ.
DR InterPro: IPR002016; Peroxidase.
DR InterPro: IPR001007; VWF_C.
DR Pfam: PF03098; An_peroxidase; 1.
DR Pfam: PF00047; IG_4.
DR Pfam: PF00560; LRR; 5.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF00093; VWC; 1.
DR PRINTS: PR00457; ANPEROXIDASE.
DR SMART: SM00409; IG; 4.
DR SMART: SM00408; IGc2; 4.
DR SMART: SM00406; IGv; 3.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00366; LRR_PS; 4.
DR SMART: SM00369; LRR_Typ; 5.
DR SMART: SM00214; VWC; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS50292; PEROXIDASE_3; 1.
DR PROSITE: PS01208; VWF_C_1; 1.
DR PROSITE: PS50184; VWF_C_2; 1.
FT NON TER 1
SQ SEQUENCE 1431 AA; 160591 MW; 6BA952436DA54B72 CRC64;

Query Match 9.5%; Score 125.5; DB 11; Length 1431;
Best Local Similarity 25.0%; Pred. No. 0.072;
Matches 57; Conservative 25; Mismatches 93; Indels 53; Gaps 9;

QY 34 GDTVELTCTASQKSIQFHWKNSNQIKLNGQSFLLTKGSKLNDKDRSRSLMDQGNF 93
DB 213 GNTVYFTCRAGEGNKPEIIMLRNN-----NELSMKTSRLNLDGT-- 254
QY LIINKLIEDSDTYICEV-----EDQKEVQLLVFGLTAN-----SDHILQGGSLTL 141
DB 94 LIINKLIEDSDTYICEV-----EDQKEVQLLVFGLTAN-----SDHILQGGSLTL 141
QY 255 LMITONTGEADBGVYQCAKNAVGAKEAKTQEVLTLYRLSSPARPTFYIQNTLEVLGSS--V 312
DB 255 LMITONTGEADBGVYQCAKNAVGAKEAKTQEVLTLYRLSSPARPTFYIQNTLEVLGSS--V 312
QY 142 TLSPSPSSPSPVQCRSPRGK-----NIQGGKTLVSQLELQDSGTWCTVLQNOK 191
DB 313 TLSPSAGHPLPQTLTWTRGRDTPPLPIDPRVITPSSGLYIQNVAGSDSGEYTCASNSVD 372
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QY 192 KVEFKIDIVPRASALP---APPTGSALPDPQT-----ASALPDPPIA 230
DB 373 SIHATAFI--VQALPQFTVTQPSRVIVIGQTVDFQCAKGHPPVIA 418

RESULT 42
Q87A95      PRELIMINARY;      PRT;      332 AA.
ID Q87A95;
AC Q87A95;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to CMRF3 antigen precursor.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC025395; AAH25395.1;
DR InterPro: IPR003599; IG_1-like.
DR InterPro: IPR007110; IG_2-like.
DR Pfam: PF00047; IG_1.
DR SMART: SM00409; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
SQ SEQUENCE 332 AA; 36059 MW; 159124621383CE93 CRC64;

Query Match 9.5%; Score 125; DB 4; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.012;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RHLLVLQALPLA--ATQGNKVLGKKDYTELCTASQK--KSIQFHWKNSNQIKLN 64
DB 2 RLVLVLMGCLLPYGALEGPBEISGFEDTVSLQTYRELRDHRKVCYCKGILFNSC 61
QY 65 QGSFLT--KPSKLNDR--DSRSLMDQGNPPLIINKLKIDSDTYICEVDQKEVQ 119
DB 62 SGTYAEEGQETMKGRVSIIRDSRQEL---SLIVTLMNLTLDAGEYWCYGEKRPDES 117
QY 120 LVFGLTANSDHLLQGSGLTLTLESPPSSPSVQCRSGRGNKIQGKTLVSQLE---- 175
DB 118 LLI-----SLFVFPGPC-----CPSPSPPTFQ-----PLATRIQPKAK 151
QY 176 -----LQDSGTWCTVLQNOKVEFKIDIVPRASAL-----PA---PPT 211
DB 152 AQQTQPPGLTSPGLVYATTAATTAQGTGAALPPLPGTSQGHERTSQYTGTSPPHATSPRA 211
QY 212 GSALPDPQ--TASALPDPPIA-----LPAALAVISFLGLGLGVAC 252
DB 212 GSSRPMPQUNSTSAEDTSPALSSGSKPVSIPWVRIILAPVLVLSLSAAGLIAC 268

RESULT 43
Q8UV81      PRELIMINARY;      PRT;      358 AA.
ID Q8UV81;
AC Q8UV81;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SC:d125023.3 (Novel immune-type receptor 1.10 (nltr1.10)).
GN SC:D125023.3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OX Cyprinidae; Danio.
RN NCBI_TaxID=7955;
RP SEQUENCE FROM N.A.
RA Garner P.;
```

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RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL591405; CADI2581.1; -.
DR GO; GO:0004872; P:receptor activity; IEA.
DR InterPro; IPR003599; 19.
DR InterPro; IPR007110; 19-like.
DR Pfam; PF00047; 19; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KM Receptor.
SQ SEQUENCE 358 AA; 40130 MW; BBAD7SEBAEAB4953 CRC64;

Query Match 9.5%; Score 125; DB 13; Length 358;
Best Local Similarity 24.1%; Pred. No. 0.013;
Matches 59; Conservative 29; Mismatches 85; Indels 72; Gaps 10;

QY 24 QGNKRVLAGKGDYELTCTASQKSIQPHM---KNSNQIKILNQGSFLTKGP----- 73
DB 56 QENNVIKIVQAGEDVNLCTFSPNQSLTAWFKHTADGKTLQIVFN--LFTKSPIMNNV 113
QY 74 SKLMDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDK-----EVOGLVFGLTAN 128
DB 114 EKMD---VNVIIIEGFNLTILKTPSDSATYIVSYQALGMGSGTRLIVDAATD 169
QY 129 SDTHLQGSFLTLTLESPGSSPSVQC-----R 156
DB 170 RNTTL--HQSLIDIVD--PGDSVNLQCSIFTESCAGDHNIYFKQSSGDSGLYTKGR 225
QY 157 SPGRKNIQGKGT-----LSVSQLLELDGSGTWCTVQLQ-----NOKVEFKIDIVP 201
DB 226 NGRCKNSAESETQSCVSLHKNNISRSPTYGYCAVACQQLLNGTQLNIRSGDLYP 285
QY 202 RASAL 206
DB 286 ALLAL 290

RESULT 44
Q9H1X9 PRELIMINARY; PRT; 390 AA.
AC Q9H1X9;
DT 01-MAR-2001 (TREMBLrel. 16; Created)
DT 01-MAR-2001 (TREMBLrel. 16; Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)
DE BG15303.1 (Similar to C.elegans hemicentin) (Fragment).
GN BG15303.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lawlor S.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL133515; CAC17584.1; -.
DR HSP; P56276; ITLK.
DR InterPro; IPR007110; 19-like.
DR InterPro; IPR003598; 19_c2.
DR Pfam; PF00047; 19; 5.
DR SMART; SM00408; IGc2; 4.
DR PROSITE; PS50835; IG_LIKE; 5.
KM Immunoglobulin domain
FT NON_TER 1
FT NON_TER 390
SQ SEQUENCE 390 AA; 42153 MW; E1F7B5D5BE6E1984 CRC64;

Query Match 9.5%; Score 125; DB 4; Length 390;
Best Local Similarity 23.3%; Pred. No. 0.014;
Matches 53; Conservative 26; Mismatches 92; Indels 56; Gaps 8;

QY 34 GDTVELTCTASQKSIQPHMKNNOIKILNQGSFLTKGPKLMDRADSRSLMDQGNF 93
DB 181 GSNVTLPCYVGYDEPTIKMRRLDMPFISR--PFSVSSISQLRTGA----- 225

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QY 94 LIINKLIEDSDTYICEVEDQ-----KEEVOGLVFGLTAN-----NSDTHLQGSFLTL 143
DB 226 LFIINLWASDKGTYICAEENQFGKIQSETTYTVGLVAPLIGISPSVANYIEGQTLPC 265
QY 144 ESPPGS-----SPSVQCRSPGRKNIQGKTLVSQLELDGSGTWCTVL 187
DB 286 TLAGNPIPERRWIKNSAMLLQNPYITVRS-----DGLHIERVQLQGGGYTCVAS 337
QY 188 Q----NOKVEFKIDIVP---RASALPAPPGSALPPQRTASALPDP 227
DB 305 NVAGTNKTKTSVVVHVLPTIQHGQQLISTEGIPVTLPCRASGNPKP 384

RESULT 45
Q96DN8 PRELIMINARY; PRT; 512 AA.
AC Q96DN8;
DT 01-DEC-2001 (TREMBLrel. 19; Created)
DT 01-DEC-2001 (TREMBLrel. 19; Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)
DE Hypothetical protein FLJ31774.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hota T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamauchi H., Chiba Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuno Y., Nagai K., Isegai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK056336; BAB71154.1; -.
DR InterPro; IPR007110; 19-like.
DR InterPro; IPR003598; 19_c2.
DR Pfam; PF00047; 19; 6.
DR SMART; SM00408; IGc2; 5.
DR PROSITE; PS50835; IG_LIKE; 6.
KM Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 512 AA; 54971 MW; 9368150E8A5D6C8 CRC64;

Query Match 9.5%; Score 125; DB 4; Length 512;
Best Local Similarity 23.3%; Pred. No. 0.021;
Matches 53; Conservative 26; Mismatches 92; Indels 56; Gaps 8;

QY 34 GDTVELTCTASQKSIQPHMKNNOIKILNQGSFLTKGPKLMDRADSRSLMDQGNF 93
DB 148 GSNVTLPCYVGYDEPTIKMRRLDMPFISR--PFSVSSISQLRTGA----- 192
QY 94 LIINKLIEDSDTYICEVEDQ-----KEEVOGLVFGLTAN-----NSDTHLQGSFLTL 143
DB 193 LFIINLWASDKGTYICAEENQFGKIQSETTYTVGLVAPLIGISPSVANYIEGQTLPC 252
QY 144 ESPPGS-----SPSVQCRSPGRKNIQGKTLVSQLELDGSGTWCTVL 187
DB 253 TLAGNPIPERRWIKNSAMLLQNPYITVRS-----DGLHIERVQLQGGGYTCVAS 304
QY 188 Q----NOKVEFKIDIVP---RASALPAPPGSALPPQRTASALPDP 227
DB 305 NVAGTNKTKTSVVVHVLPTIQHGQQLISTEGIPVTLPCRASGNPKP 351

RESULT 46
Q9VCT4 PRELIMINARY; PRT; 545 AA.
AC Q9VCT4;
DT 01-MAY-2000 (TREMBLrel. 13; Created)
DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)

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DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 DE Klg protein (LBD10776P).  
 GN Klg OR C66669.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 ON NCBI\_taxid=7227;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Aamane M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolniskov S.,  
 RA Borkova D., Botchan M.R., Boulter J., Brokstein P., Brotlier P.,  
 RA Burdick K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Dey A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fodor B.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ileguam C.,  
 RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kienison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laslo P., Lei Y., Levtitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclet J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Raintett K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Slater E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RU [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=Berkley;  
 RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Paclet J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003741; AAF56071.1; -  
 DR EMBL; AY060363; AAL25402.1; -  
 DR FlyBase; FBgn0017590; klg.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; Ig\_3.  
 DR SMART; SM00408; IG2; 3.  
 DR SMART; SM00408; IG2; 3.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 545 AA; 60087 MW; DSE81D9E5574E9DE CRC64;

Query Match 9.5%; Score 125; DB 5; Length 545;  
 Best Local Similarity 22.3%; Pred. No. 0.022;  
 Matches 50; Conservative 36; Mismatches 100; Indels 38; Gaps 8;  
 QY 2 NNGVPRHLLVLTAL-----LPAATQGNKVVLGKKGDTVELTCTASQKSIQFMH 53  
 DB 75 NNGSNRSMSNVQGSVAVALTLATLPRFLSGHTRAVAGDTLVPCQVENGNVLLM 134  
 QY 54 KNSNQIKLGNQGSFLTKGPSKLNDRASRSRLMDQGNFPLIKLKIEDSDTICEV-- 111  
 DB 135 RRGTVLTLASN--IMVTR-----DERVRLID--GYNLEISDLPEODAGDYVOCID 181  
 QY 112 ---EDQKEVQL-----VGLTANSPHTLLQGSLLTLTSPGSSPSVQCRSPRKN-- 162  
 DB 182 KINRDVHTVELVLPSPVAIFPSGQLQARKGGPITLCKGSGNPVSIWTYKSGANMS 241  
 QY 163 ---IQGKTLVSQLELDQSGTWTCV---LQNKVREFRIDV 200  
 DB 242 TARIGDPLITLTKLERQAGVYQCTADNGVDPTVDMRLDVL 285  
 RESULT 47  
 ID 096RW7 PRELIMINARY; PRT; 5636 AA.  
 AC 096RW7;  
 DT 01-DEC-2001 (TEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
 DE Hemolentin.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_taxid=9606;  
 RP SEQUENCE FROM N.A.  
 RC Trent J.;  
 RT "Human hemolentin gene.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF156100; AA68690.1; -  
 DR GO; GO:0005727; C:extrachromosomal circular DNA; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR00875; Cecropin.  
 DR InterPro; IPR01434; DUF1.  
 DR InterPro; IPR01881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_1like.  
 DR InterPro; IPR009017; GFP\_1like.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR InterPro; IPR000169; SH3prot\_acalte.  
 DR InterPro; IPR000884; TSP1.  
 DR InterPro; IPR002035; VWF\_A.  
 DR Pfam; PF00008; EGF\_5.  
 DR Pfam; PF00047; Ig\_44.  
 DR Pfam; PF00090; tSP\_1; 6.  
 DR SMART; SM00179; EGF\_Ca; 7.  
 DR SMART; SM00408; IG2; 43.  
 DR SMART; SM00209; TSP1; 6.  
 DR SMART; SM00327; VWA; 1.  
 DR TIGRFAMs; TIGR01451; B ant repeat; 9.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 5.  
 DR PROSITE; PS00268; CECROPIN; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 8.  
 DR PROSITE; PS50835; IG\_LIKE; 44.  
 DR PROSITE; PS00639; TH1OL\_PROTEASE\_HIS; 1.  
 DR PROSITE; PS50092; TSP1; 6.  
 KW EGF-like domain; Immunoglobulin domain.  
 SQ SEQUENCE 5636 AA; 613660 MW; F000B319CED7B52C CRC64;  
 Query Match 9.5%; Score 125; DB 4; Length 5636;

Best Local Similarity 23.3%; Pred. No. 0.48;  
Matches 53; Conservative 26; Mismatches 92; Indels 56; Gaps 8;

```

OY 34 GDTVELTCTASQKSIQCHMKNSNOIKILGNQGSFLTGPSTLNDRAISRSLMDQNF 93
Db 807 GSNVTLPCYVOGYEPTIKMRLDMPIFSR--PFSVSSISQLRTGA----- 851
OY 94 LIKKLKIEDSDTYICEVEDQ-----KEEVQLVFLTLA-----NSDTHLQGSFLTL 143
Db 852 LPIALNMSDKGTICENQNGKIQSETTYVTGLVPLGISVSNVIEGQQLLPC 911
OY 144 ESPSGS-----SPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWCTVL 187
Db 912 TLGNPNPIPERRMKNSAMLQNPITYRS-----DGLHIERVOLQDQGEVTCVAS 963
OY 188 Q----NOKKVEFKIDIV---RASALPAPPTGSALPDQOTASALPD 227
Db 964 NVAGTNNKTSVVAHVLEPTIOHQOILSTIEGIPVTLCKASGNPKP 1010

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## RESULT 48

```

ID 09EQK9 PRELIMINARY; PRT; 394 AA.
AC 09EQK9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE NK cell receptor 2B4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PVG;
RX MEDLINE=21173196; PubMed=11275258;
RA Kumarasan P.R., Stepp S.E., Verreut P.C., Chuang S.S., Boles K.S.,
RA Lai W.C., Ryan J.C., Bennett M., Kumar V., Mathew P.A.;
RT "Molecular characterization of the rat NK cell receptor 2B4.";
RL Mol. Immunol. 37:735-744(2000).
DR EMBL; AF209406; AAC35766.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
SQ SEQUENCE 394 AA; 44286 MM; 6F917EF02C542198 CRC64;

```

Query Match 9.5%; Score 124.5; DB 11; Length 394;  
Best Local Similarity 21.1%; Pred. No. 0.016; Matches 92; Indels 115; Gaps 12;  
Matches 64; Conservative 33; Mismatches 92; Indels 115; Gaps 12;

```

OY 12 LVQLALPLPAATOG-----NKVVLGKKGDTVELTCTASQKSIQCHMKNSNOIKILGNQ 65
Db 6 VLISLFLLRHQGDGAGSSEBVLGVGKPRRLRPSNIQTKHSIEK----- 54
OY 66 GSFLTKGSKLNDRAISRSLMDQNF 107
Db 55 -----KKTGHQOTSHIVMTNLDPESPVCCSDIYGFESFENFALSIKAKINDSGHY 106
OY 108 ICEVEDQ-----KEEVQLVFLTLA-----NSDTHLQGSFLTLTLESPPSS 150
Db 107 LLEITDQGGIVCTKFOILFDPVETPHLTVQGSIMANGTQL----- 149
OY 151 PSVQCRSPRGKNI-----QGGKTLVSQ-----LELDQSGTWCTVLNOKKVEFKI 197
Db 150 -SLGCFVXKDNVNSALYRGSMILSNQNGHWMEMDASSLHYTCVNSK----- 200
OY 198 DIVPRASALPAPPTGSALPDQOTASALPDPAASALPALAV---ISFLGLGLGACVL 254
Db 201 -----ASWANHITLSPQSCQSVS--KFNVLPPVVISGILVTFLLG-ALACFCW 247
OY 255 ARTR 256

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Db 248 NRKR 251

## RESULT 49

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ID 098923 PRELIMINARY; PRT; 504 AA.
AC 098923;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE HEMCAM precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H.B190V+; TISSUE=Thymus;
RX MEDLINE=97133433; PubMed=8978830;
RA Vainio O., Dunon D., Alsel F., Dangy J.P., McNaghy K.M., Imhof B.A.;
RT "HEMCAm, an adhesion molecule expressed by c-kit+ progenitors.";
RL J. Cell Biol. 135:1655-1668(1996).
DR EMBL; Y08854; CA70079.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 35
FT CHAIN 36 504
FT SEQUENCE 504 AA; 55540 MM; ADAE4B94ED4F02E1 CRC64;

```

Query Match 9.5%; Score 124.5; DB 13; Length 504;  
Best Local Similarity 23.7%; Pred. No. 0.022; Matches 88; Indels 43; Gaps 6;  
Matches 50; Conservative 30; Mismatches 88; Indels 43; Gaps 6;

```

OY 19 LPAATQGNKVVYLGKKGDTVELTCTASQKSIQCHMKNSNOIKILGNQGSFLTKGPKSLND 78
Db 268 LRVATNAGIV---KEGDVYKVCAD-----GNPAPVPSFRRRLGD 306
OY 79 RADSRSLMDQNFPLIILKLIKIEDSDTYICEVED-----QKEVQLV-----FGL 125
Db 307 SWQDMTSLADTNDGVLMILHNVSQSSGLYRCQTLDDMTQHEGDELVNVYIEGVQVKM 366
OY 126 TANSDTHLQGSFLTLTLESPPSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWCT 185
Db 367 EPSSPFLH--EGDSYRLCTAHSPYKLDYQWRDARGRYAEGNQLTLNLTFTETSSNFSR 424
OY 186 V-----LONOKKVEFKIDIVPRASALPAP 209
Db 425 VKARSVPGLGSKQVAVAVKGRIVAVISAP 455

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## RESULT 50

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ID 098921 PRELIMINARY; PRT; 584 AA.
AC 098921;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE HEMCAM precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H.B190V+; TISSUE=Thymus;
RX MEDLINE=97133433; PubMed=8978830;

```

RA Vainio O., Dunon D., Aisai F., Dangy J.P., McNaghy K.M., Imhof B.A.:  
 RT "HEMCM" an adhesion molecule expressed by c-kit<sup>+</sup> progenitors.";  
 DR J. Cell Biol. 135:1655-1668(1996).  
 DR EMBL: Y08856; CAA70081.1; -  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR Pfam: PF00047; Ig; 5.  
 DR SMART: SM00408; Igc2; 1.  
 DR PROSITE: PSS0835; IG-LIKE; 5.  
 DR KIM: Immoglobulin domain; Signal.  
 FT SIGNAL 1 35  
 FT CHAIN 36 584  
 SO SEQUENCE 584 AA; 64422 MW; 5972D946604AF6F3 CRC64;

Query Match 9.5%; Score 124.5; DB 13; Length 584;  
 Best Local Similarity 23.7%; Pred. No. 0.027;  
 Matches 50; Conservative 30; Mismatches 88; Indels 43; Gaps 6;

QY 19 LPAATQGNKRVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNGQSFLTGPSTKLAND 78  
 DB 268 LRAVATNAGIV---KEGDVAVLCDDA-----GNPAPVPSFPRRELGD 306  
 QY 79 RADSRRLMDQGNFPLIINKLIKEDSDTYICEVED-----OKEEVQLLV-----FGL 125  
 DB 307 SWQDMTSLADTNDGVLMHNVSXSSGLYRCQTLDDMTQHEGDVELVNNYIEGVQVKM 366  
 QY 126 TANSPTHLQGSGLTTLTLESPSSPVQCRSPRGKNIQSGKTLVSQLELDQSGTWCT 185  
 DB 367 EPSSPLH--EGDSVRLSCTAHSPVKLDYQWRDARGKVAEGNQLLTNLTFETSSNFSR 424  
 QY 186 V-----LONOKVEFKIDIVPRASALPAP 209  
 DB 425 VKARSVPGLEQSKQVAVAVGKPRIVAIISAP 455

## RESULT 51

Q09089 PRELIMINARY; PRT; 584 AA.  
 AC Q09089;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE S-gicerin.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Leghorn; TISSUE=Gizzard;  
 RX MEDLINE=94213753; PubMed=8161457;  
 RA Taira E., Takaha N., Taniura H., Kim C., Miki N.;  
 RT "Molecular cloning and functional expression of gicerin, a novel cell  
 adhesion molecule that binds to neurite outgrowth factor.";  
 RL Neuron 12:861-872(1994).  
 RT [2]  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Leghorn; TISSUE=Gizzard;  
 RX MEDLINE=96081930; PubMed=7499388;  
 RA Taira E., Negino T., Taniura H., Takaha N., Kim C., Kuo C., Li B.,  
 RA Higuchi H., Miki N.;  
 RT "Expression and functional analysis of a novel isoform of gicerin, an  
 immunoglobulin superfamily cell adhesion molecule.";  
 RL J. Biol. Chem. 270:28681-28687(1995).  
 DR EMBL: D38559; BAA07563.1; -  
 DR PIR: I50419; I50419.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR Pfam: PF00047; Ig; 4.  
 DR SMART: SM00408; Igc2; 1.  
 DR PROSITE: PSS0835; IG-LIKE; 4.  
 KW Immunoglobulin domain.

SO SEQUENCE 584 AA; 64378 MW; 876E0C3E920BA92F CRC64;

Query Match 9.5%; Score 124.5; DB 13; Length 584;  
 Best Local Similarity 23.7%; Pred. No. 0.027;  
 Matches 50; Conservative 30; Mismatches 88; Indels 43; Gaps 6;

QY 19 LPAATQGNKRVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNGQSFLTGPSTKLAND 78  
 DB 268 LRAVATNAGIV---KEGDVAVLCDDA-----GNPAPVPSFPRRELGD 306  
 QY 79 RADSRRLMDQGNFPLIINKLIKEDSDTYICEVED-----OKEEVQLLV-----FGL 125  
 DB 307 SWQDMTSLADTNDGVLMHNVSXSSGLYRCQTLDDMTQHEGDVELVNNYIEGVQVKM 366  
 QY 126 TANSPTHLQGSGLTTLTLESPSSPVQCRSPRGKNIQSGKTLVSQLELDQSGTWCT 185  
 DB 367 EPSSPLH--EGDSVRLSCTAHSPVKLDYQWRDARGKVAEGNQLLTNLTFETSSNFSR 424  
 QY 186 V-----LONOKVEFKIDIVPRASALPAP 209  
 DB 425 VKARSVPGLEQSKQVAVAVGKPRIVAIISAP 455

## RESULT 52

Q08922 PRELIMINARY; PRT; 626 AA.  
 AC Q08922;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE HEMCAM precursor.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H-B19ov+; TISSUE=Thymus;  
 RX MEDLINE=97133433; PubMed=8978830;  
 RA Vainio O., Dunon D., Aisai F., Dangy J.P., McNaghy K.M., Imhof B.A.;  
 RT "HEMCM, an adhesion molecule expressed by c-kit<sup>+</sup> progenitors.";  
 RL J. Cell Biol. 135:1655-1668(1996).  
 DR EMBL: Y08855; CAA70080.1; -  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR Pfam: PF00047; Ig; 5.  
 DR SMART: SM00408; Igc2; 1.  
 DR PROSITE: PSS0835; IG-LIKE; 5.  
 KW Immunoglobulin domain; Signal.  
 FT SIGNAL 1 35  
 FT CHAIN 36 626  
 SO SEQUENCE 626 AA; 69104 MW; 27F8F2F47044E163 CRC64;

Query Match 9.5%; Score 124.5; DB 13; Length 626;  
 Best Local Similarity 23.7%; Pred. No. 0.03;  
 Matches 50; Conservative 30; Mismatches 88; Indels 43; Gaps 6;

QY 19 LPAATQGNKRVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNGQSFLTGPSTKLAND 78  
 DB 268 LRAVATNAGIV---KEGDVAVLCDDA-----GNPAPVPSFPRRELGD 306  
 QY 79 RADSRRLMDQGNFPLIINKLIKEDSDTYICEVED-----OKEEVQLLV-----FGL 125  
 DB 307 SWQDMTSLADTNDGVLMHNVSXSSGLYRCQTLDDMTQHEGDVELVNNYIEGVQVKM 366  
 QY 126 TANSPTHLQGSGLTTLTLESPSSPVQCRSPRGKNIQSGKTLVSQLELDQSGTWCT 185  
 DB 367 EPSSPLH--EGDSVRLSCTAHSPVKLDYQWRDARGKVAEGNQLLTNLTFETSSNFSR 424  
 QY 186 V-----LONOKVEFKIDIVPRASALPAP 209  
 DB 425 VKARSVPGLEQSKQVAVAVGKPRIVAIISAP 455

## RESULT 53

Q90880 PRELIMINARY; PRT; 626 AA.  
 AC Q90880;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE L-gicerin.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Lehman; TISSUE=Gizzard;  
 RX MEDLINE=6081930; PubMed=749938;  
 RA Taira E., Nagino T., Tanura H., Takaha N., Kim C., Kuo C., Li B.,  
 RA Hsiueh H., Miki N.,  
 RT "Expression and functional analysis of a novel isoform of gicerin, an  
 immunoglobulin superfamily cell adhesion molecule."  
 RL J. Biol. Chem. 270:28681-28687 (1995).  
 DR EMBL; D49849; BAA08648.1; -  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig\_4.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 KM Immunoglobulin domain.  
 SQ SEQUENCE 626 AA; 69074 MW; C4791BECCE55133 CRC64;

Query Match 9.5%; Score 124.5; DB 13; Length 626;  
 Best Local Similarity 23.7%; Pred. No. 0.03;  
 Matches 50; Conservative 30; Mismatches 88; Indels 43; Gaps 6;  
 QY 19 LPATQGNKVVLGKKDPTVELTCTASQKSIQFHMKNNOIKLGNQSGFLTKGPSKLTND 78  
 DB LRVATNAGIV--KEGDVVKLVCDAD-----GNPAPVFSFRRRLGD 306  
 QY 79 RADRRSLMDQGNFPLIKIKIEDPTVCEVED-----QKEEVOLLV-----FGL 125  
 DB 307 SMDQMTSLADTNDGVLMLHNVSKSSGILRCQITLDLDMTHQEDVELVAVYITGVQVM 366  
 QY 126 TANSDFHLLQGSILTLTLESPGSSPSVQCRSPKNIQGGKTLISVQLELQDSGTWCT 185  
 DB 367 EPSSPLH--EGDSVRLSCTAHSPVKLDYQWRDARGKVAEGNQLLTTLTFTETSSNFSR 424  
 QY 186 V-----LONQKVEPKIDIVPRASALPAP 209  
 DB 425 VKARSVPGLEQSKQVAVAVKGPRIAVISAP 455

## RESULT 54

Q9NR99 PRELIMINARY; PRT; 2828 AA.  
 AC Q9NR99;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Adican.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA Crowl R.M., Luk D.,  
 RT "Identification of the gene encoding Adican, a novel protein  
 expressed in human arthritic tissues."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF245505; AAF66402.1; -  
 DR HSSP; P56276; ITLK.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003591; LRR\_Cyp.  
 DR Pfam; PF00047; Ig\_12.  
 DR Pfam; PF00560; LRR; 6.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR SMART; SM00408; IGC2; 10.  
 DR SMART; SM00082; LRRCT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR SMART; SM00369; LRR\_TYR; 3.  
 DR PROSITE; PS50835; IG\_LIKE; 12.  
 KM Immunoglobulin domain.  
 SQ SEQUENCE 2828 AA; 312291 MW; A18377D8554F1FE1 CRC64;

Query Match 9.5%; Score 124.5; DB 4; Length 2828;  
 Best Local Similarity 23.1%; Pred. No. 0.21;  
 Matches 56; Conservative 36; Mismatches 83; Indels 67; Gaps 12;  
 QY 22 ATQGNKVVLGKKDPTVELTCTASQKSIQFHMKNNOIKLGNQSGFLTKGPSKLTND 81  
 DB 484 AVGRDQTVL--EGRPQLSCNVKASEPSIFW-----VLPD-GSIL-KAPM---DDPD 529  
 QY 82 SRRLMDQGNFPLIKIKIEDPTVCEVEDQKEVOLLVFGITANSDFHLLQGSILTL 141  
 DB 530 SKFSILSSG--WLRIKMEPSDSGLYOC-IAQVRDEMDRMVRYLVQSPS--TQPAERDV 585  
 QY 142 TLSEPPSSPSVQCRS-----PRKNIQGGKTLISV 171  
 DB 586 TIGKNPESVTLPCNALAIPKALSWILPNRIINDIANTSHVYMLNG-----TLST 638  
 QY 172 SOLELQSGTWTCTVLOQKVEPKIDIVPRASALPAPPTGSALPDPTASALPDPPAAS 231  
 DB 639 PKVQVSSSGYRCVAVVQAGADHTVGIT-----VTKQSGSLPSRGRR-----FGAK 686  
 QY 232 AL 233  
 DB 687 AL 688

## RESULT 55

Q8UV52 PRELIMINARY; PRT; 325 AA.  
 AC Q8UV52;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE SC:d2263J20.6 (Novel immune-type receptor).  
 GN SC:D2263J20.6.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hammond S.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL591476; CAD21600.1; -  
 DR GO; GO:0004872; F:receptor activity; IBA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig\_2.  
 DR SMART; SM00409; IG\_2.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 KM Receptor.  
 SQ SEQUENCE 325 AA; 36190 MW; 01F5BCE2055EE064 CRC64;

Query Match 9.4%; Score 124; DB 13; Length 325;

Best Local Similarity 23.7%; Pred. No. 0.014;  
Matches 57; Conservative 33; Mismatches 88; Indels 64; Gaps 9;

QY 24 QGNKVVYLGKKKDTVELTCTASQKKSIOFHW-----KNSNQIKLGNQSGFLTKGSPSKLN-- 77  
DB 23 QENNVKIVQAGEDVNLCTFSNNWQLSTAFMKHTADGKTLQIVFN--LFFTKSPIMNNV 80  
QY 78 DRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEQK-----EYQVLVFGILANSDPH 132  
DB 81 EKNMNVVVIIEEGFNLTKTKPSDAIYCVVSSVQAIQMGSGTLLIVRADATDRNTT 140  
QY 133 LIGQSLTLTSSPGSSPSVQC-----RSPRG 160  
DB 141 L--HQSLIDTVD--PGSVNLQCSIFTESCAGDSHYWFKQSGDSEGVLYTKGERANGNC 196  
QY 161 KNIQGGKT-----LSVSQLELDGSGTCTCTVQ-----NKKVEFKDIVPRASA 205  
DB 197 KNSAESPTQSCVYSLHKMNISRSDDTYIYCAVAACQIILGNQTQINIRESGDLYPALTA 256  
QY 206 L 206  
DB 257 L 257

RESULT 56  
ID 063669 PRELIMINARY; PRT; 739 AA.  
AC 063669;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Vascular cell adhesion molecule 1 precursor.  
GN VCAM-1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague Dawley; TISSUE=Lung;  
RX MEDLINE=92305064; PubMed=1377031;  
RA Williams A.J., Atkins R.C., Fries J.W., Gimbrome M.A.Jr.,  
RA Cybulsky M.J., Collins T.;  
RT "Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA.";  
RL Biochim. Biophys. Acta 1191:214-216(1992).  
DR EMBL; X63722; CAA45254.1; -;  
DR HSSP; P19320; IVCA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016337; P:cell-cell adhesion; IEA.  
DR InterPro; IPR003987; ICAM VCAM-1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig-C2.  
DR InterPro; IPR003989; VCAM-1.  
DR Pfam; PF00047; Ig\_5.  
DR PRINTS; PRO1472; ICAMVCAM1.  
DR PRINTS; PRO1474; VCAM1.  
DR SMART; SM00408; ICG2; 4.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
KW Immunoglobulin domain; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 739 VASCULAR CELL ADHESION MOLECULE 1.  
SQ SEQUENCE 739 AA; 81136 MW; ASAAD1172F67F9B6 CRC64; /

Query Match 9.4%; Score 124; DB 11; Length 739;  
Best Local Similarity 23.4%; Pred. No. 0.041;  
Matches 43; Conservative 30; Mismatches 71; Indels 40; Gaps 5;

QY 33 KGDVVELTCTASQKKSIOFHWKNSNQIKLGNQSGFLTKGSPSKLNDRADSRSLMDQGNF 92  
DB 238 EGAAVVTCTASGEGIPAPETFSKR-----LDNGVQLQ-----SGNA 274  
QY 93 PLIKNLKIEDSDTYICEVEQK-----VEDQKEVQLLV-----FGLTANSDPHLLQSGSLTLT 142

DB 275 TLTLIAMRMEDSGIYVCEGNVLVGRDKTEVELLVOEKPTVDISPSQVAAQVDSVLT 334  
QY 143 LESPPSSSVCCRPGRKNIG-----GTLISVSQLELDGSGTCTCTVQGNKKVEF 195  
DB 335 CAVQCDSPSSFSMRQTDSPLNGEVRDEGATSTLTLSPGVDEHSDLYCTVQCRKLEK 394  
QY 196 KIDI 199  
DB 395 TIQV 398

RESULT 57  
ID 09VLF0 PRELIMINARY; PRT; 532 AA.  
AC 09VLF0;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE CG31708-PA (CG31708-PB).  
GN CG31708.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazer J.G., Chame M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gaber G.L.,  
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu B., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokov D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K.J., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Galbraith W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jajalji M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Moberly C., Morris J., Mosherfi A.,  
RA Mount S.M., Moy W., Murphy B., Murphy L., Murthy D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svitek R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodagert, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,  
RA Clamp M.E., Drysdale R.A., Emmert D., Fries E., de Grey A.D.N.J.,  
RA Harris N.L., Krommiller B., Marshall B., Milburn G.H., Richter J.,

RA Ruoso S., Searle S.M.J., Smith E., Shu S., Smurniak F.,  
 RA Whitefield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,  
 RA Lewis S.E.;  
 RT "Annotation of Drosophila melanogaster genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN (4)  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB003623; AAF52743.3; -  
 DR FlyBase; FBgn0051708; CG31708.  
 DR InterPro; IPR003599; IG\_1.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; IG\_2.  
 DR SMART; SM00409; IG\_3.  
 DR SMART; SM00408; IGC2; 3.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 SO SEQUENCE 532 AA; 56872 MW; 67D3D39A270FE22E CRC64;

Query Match 9.3%; Score 122.5; DB 5; Length 532;  
 Best Local Similarity 20.8%; Pred. No. 0.036; Indels 41; Gaps 7;  
 Matches 47; Conservative 41; Mismatches 97;

QY 5 VPFHLLVLQALLPAATQGNKVVLLGKGGDTVELTCTASQKSIQFHMKNNOIKILGN 64  
 DB 101 VPTSNLNIIVE--EPEFTYIENVTYPAGRNVKLGSGVKMIGSKVAMHMFESALITV 157  
 QY 65 QGSFLTKGP--SKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQLLV 122  
 DB 158 HNHVITRNPRISVTHDKIDRHRWY-----LHNNVHEEDRGRCMCOINTVTKTQ--- 208  
 QY 123 FGL-----TANSDPHLQGGSLTLTLSPSSPSVOCSPRGKNIQ----- 164  
 DB 209 FGYNLVVVPPIIDSLSSDIYREGANISLRCASSGPRPIIKKRDNSRIAINKNI 268  
 QY 165 ---GKTLVSQLELQDSGTWCTVLON-----QKVEFKIDIVP 201  
 DB 269 VNEWEGDTLEITRISRLDMGAYVLCTASNGVPTVSKRIKVSVDPP 314

## RESULT 58

Q723B1 PRELIMINARY; PRT; 355 AA.

AC Q723B1;  
 DT 01-OCT-2003 (Tremblrel. 25, Created)  
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Hypothetical protein DKFZp686B1946 (Fragment).  
 GN DKFZp686B1946.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCB1\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Human amygdala;  
 RA Amosges W., Krieger S., Regiert T., Rittmuller C., Schwager B.,  
 RA Meyer H.W., Weill B., Andl C., Osanger A., Fobo G., Han W., Wiemann S.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX538014; CAD97961.1; -  
 KM Hypothetical protein.  
 FT NON TER  
 SO SEQUENCE 355 AA; 38776 MW; 67CA5457F160FAD15 CRC64;

Query Match 9.3%; Score 122; DB 4; Length 355;  
 Best Local Similarity 23.0%; Pred. No. 0.023;  
 Matches 53; Conservative 36; Mismatches 93; Indels 48; Gaps 10;

QY 20 PAATQGNKVVLLGKGGDTVELTCTASQKSIQFHMKNNOIKILGNQGSFLTKGP-----SK 75  
 DB 42 PMAVDMMV--RKGDTAVLRCTYEDGAS--KGALNNSSTIFAG--GDKMSVDRVSI 96  
 QY 76 LNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQLLVFGLTA----- 127  
 DB 97 LNKR-----DYSLQIQNVDTVDGPGYTCVQHTPRTMQYH-LTVQVPPKIYD 144  
 QY 128 -NSDTHLQGSLLTLTSPSSPSVQCR--SPRGNIQGKTLVSQLELQDSGTWCT 184  
 DB 145 ISNDTVNEGTVTLTCLATGKPPPSISWRHISPAKPFENGQYLDITGTRDQAGEYC 204  
 QY 185 TV-----LQNKVEFKIDIVPRASALPAPT-----GSALPDP 218  
 DB 205 SAENDVSPDVPRKVKVNVNFAPTIQEIKSGVTYGRSGLRCEAGVPPP 254

## RESULT 59

O93250 PRELIMINARY; PRT; 1009 AA.

AC O93250;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Contactin A.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCB1\_TaxID=8355;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=J; TISSUE=Brain;  
 RA Nagata S., Suzuki A.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=J; TISSUE=Brain;  
 RA Nagata S., Fujita N., Takeuchi K., Watanabe K.;  
 RT "cDNA cloning and expression of the Xenopus homologue of the neural  
 cell adhesion molecule, contactin (p3/Fl1).";  
 RL Zool. Sci. 13:813-820(1997).  
 DR EMBL; AB015205; BAA28780.1; -  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; FN3; 4.  
 DR Pfam; PF00047; IG; 6.  
 DR SMART; SM00060; FN3; 4.  
 DR SMART; SM00408; IGC2; 3.  
 DR PROSITE; PS50835; IG\_LIKE; 6.  
 KM Immunoglobulin domain.  
 SO SEQUENCE 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64;

Query Match 9.3%; Score 122; DB 13; Length 1009;  
 Best Local Similarity 21.5%; Pred. No. 0.092; Indels 64; Gaps 7;  
 Matches 51; Conservative 28; Mismatches 94;

QY 11 LTVLQALLPAATQGNKVVLLGKGGDTVELTCTASQKSIQFHMKNNOIKILGNQGSFLT 70  
 DB 392 LKIALAPTEFTPMRKVLAAGKRVYIECKRAKAFKFSKGTLELI----- 442  
 QY 71 KGPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQ-LVFGLTANS 129  
 DB 443 -----NNSRYSIIDDS--LEIINIKLDEGSGYCAENDRGANGTAVLSVTAAT 491  
 QY 130 DTHLQGSLLTLTSPSSPSVQCR----- 155  
 DB 492 KITLAPSA-----DYTVGENATMQCNASHDPTLDLSYISLNGFPIEFMEDRHYERAI 546  
 QY 156 RSPRGNIQGKTLVSQLELQDSGTWCTVLONQKVEFKIDIVPRASALPAPTPT 212

Db 547 RLPLQNDV--GSELLIKNAOLKAHGRVTCMTQTLVNDSSASADLVVAGP--RGPFG 599

RESULT 60

ID	Q88HV1	PRELIMINARY;	PRT;	885 AA.
AC	Q88HV1			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	glycosylphosphatidylinositol anchor 1 protein (Fragment).			
GN	MDGAL.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kierseisen S., Al-Bayati H., Kollers S., Brenig B.;			
RT	"Assignment of the porcine MAM domain containing			
RT	glycosylphosphatidylinositol anchor 1 (mdgal) on chromosome 7q11-13 by			
RL	in situ hybridisation."			
RL	Submitted (OCT-2002) to the EMBL/Genbank/DBJ databases.			
EMBL:	AL459296; CAD30702.2; -			
GO:	GO:0016020; C:membrane; IFA.			
DR	InterPro; IPR008957; FN_III-like.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-1-like.			
DR	InterPro; IPR003598; IG_c2.			
DR	InterPro; IPR000998; MAM_domain.			
DR	Pfam; PF00047; Ig_5.			
DR	Pfam; PF00629; MAM_1.			
DR	PRINTS; PR00020; MAMDOMAIN.			
DR	SMART; SM00409; IG_5.			
DR	SMART; SM00137; MAM_1.			
DR	PROSITE; PSS0835; IG LIKE; 5.			
DR	PROSITE; PSS0060; MAM_2; 1.			
FT	NON TER 1			
SQ	SEQUENCE 885 AA; 97766 MW; BC2929D59C43491C5 CRC64;			

Query Match 9.2%; Score 121; DB 6; Length 885;  
 Best Local Similarity 26.3%; Pred. No. 0.094;  
 Matches 47; Conservative 24; Mismatches 66; Indels 42; Gaps 7;

ID	Q88HV2	PRELIMINARY;	PRT;	886 AA.
AC	Q88HV2			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	MAM domain containing glycosylphosphatidylinositol anchor 1			
DE	(Fragment).			
GN	MDGAL.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			

RESULT 61

ID	Q88HV2	PRELIMINARY;	PRT;	886 AA.
AC	Q88HV2			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	MAM domain containing glycosylphosphatidylinositol anchor 1			
DE	(Fragment).			
GN	MDGAL.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			

RP SEQUENCE FROM N.A.  
RA Klerstein S., Al-Bayati H., Koller S., Brenig B.;  
RT "Assignment of the porcine MAM domain containing  
RT glycosylphosphatidylinositol anchor 1 (MDA1) on chromosome 7q11-q13  
RT by in situ hybridization."  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ459295; CAD30701.2; -.  
DR GO: GO:0016020; C:membrane; IEA.  
DR InterPro: IPR008957; FN\_III-like.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003598; IG\_c2.  
DR InterPro: IPR000998; MAM\_domain.  
DR Pfam: PF00047; IG\_5.  
DR Pfam: PF00629; MAM; 1.  
DR PRINTS: PRO0020; MAMDOMAIN.  
DR SMART: SMO0409; IG; 5.  
DR SMART: SMO0408; IGc2; 5.  
DR SMART: SMO0137; MAM; 1.  
DR PROSITE: PSS0835; IG\_LIKE; 5.  
DR PROSITE: PSS0060; MAM\_2; 1.  
FT NON TER 1  
SQ SEQUENCE 886 AA; 98074 MW; B69872711DB9D52 CRC64;

Query Match 9.2%; Score 121; DB 6; Length 886;  
Best Local Similarity 26.3%; Pred. No. 0.095;  
Matches 47; Conservative 24; Mismatches 66; Indels 42; Gaps 7;

Qy 36 TVELTCTASOKKSIQFMKNSNOIKILGNQGSFLTKGPSKLANDRADSRSLMDQGNFPLI 95  
Db 83 TVFLRCTVNSNPAPRFVTKKGS-----TLHSQDNG-VDIYEPLVYQGAEVL 130  
Qy 96 -IKNLIKEDSDTYICEVED-----QKEVQLLVFGLTANSDFHLQGSGLTTLLESPPG 148  
Db 131 KIKLRQREYASLTICQVDSGVCIGPKAVTLRLTSTTAPALML-----SVNETLVNPG 186  
Qy 149 SSEPVOC-----RRPRKNIQGGKTLTSVSLQELDQSGTWCTVQLN 189  
Db 187 ENVTQCLLQGGDPLTQLQWSHGPGPLPLGALAQG-TLISPVQARDSGVYNCTATNN 244

RESULT 62  
P79921 PRELIMINARY; PRT; 1005 AA.  
ID P79921  
AC P79921;  
DT 01-MAY-1997 (Tremblrel. 03, Created)  
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Contactin/F3/F11.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodidae; Xenopus.  
CX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J strain; TISSUE=Brain;  
RA Nacata S., Fujita N., Takeuchi K., Watanabe K.;  
RT "cDNA cloning and expression of the Xenopus homologue of the neural  
RT cell adhesion molecule, contactin (F3/F11).";  
RL Zool. Sci. 13:813-820 (1997).  
DR EMBL: D86505; BAAL3100.1; -.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR008957; FN\_III-like.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003598; IG\_c2.  
DR Pfam: PF00041; fn3; 4.  
DR Pfam: PF00047; IG; 6.  
DR SMART: SMO0060; FN3; 4.  
DR SMART: SMO0408; IGc2; 5.  
DR PROSITE: PSS0835; IG\_LIKE; 6.  
KW Immunoglobulin domain.  
SQ SEQUENCE 1005 AA; 111665 MW; 6F1CE811FBD97DFE CRC64;



```

Query Match      9.1%; Score 120; DB 13; Length 1005;
Best Local Similarity 21.6%; Pred No. 0.14;
Matches 51; Conservative 28; Mismatches 91; Indels 66; Gaps 7;

OY 11 LVLQALPPATQGNKRVLGKGGDTVELTCTASQKSAIQFHWKNSNOIKILNGQSGFLT 70
DB 392 LKILALAPTEFTPPKRVKYLAKGGRVILECKPKAPAPKAFWSKSTGLTLL----- 442
OY 71 KPSKLTNRADSRSLNMQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLVFGILTANS 130
DB 443 -----NNSRVSIMWDS--LEITNITKFEDESGSYTCFAMDRGK-----ANS- 481
OY 131 THLGQSGSLTTLTEPP-----GSSPSVQCRSPRGKNIQ----- 164
DB 482 TGIYSVTATKITTLAPSNADVTGGENATMOCHASHDPTLELFTWALNGFIEFDKXGH 541
OY 165 -----GKTLVSQLELODSGTWCTCTVLONQKKEFKIDIVPRASALPAPPTG 212
DB 542 YERAIRNVVGSSELVIKNQQLIHAGRYTCTAQTIVNSSASADLVLRGP--FGPRGG 595

RESULT 63
ID P70193 PRELIMINARY; PRT; 1091 AA.
AC P70193;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Membrane glycoprotein.
GN LRIG1 OR IMG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96394313; PubMed=8798419;
RT "cDNA cloning of a novel membrane glycoprotein that is expressed
RT specifically in glial cells in the mouse brain LIG-1: A protein with
RT leucine-rich repeats and immunoglobulin-like domains."
RL J. Biol. Chem. 271:22522-22527(1996).
DR EMBL: D78572; BA11416.1; -.
DR PIR: A58532; A58532.
DR HSSP; P56276; 1TLK.
DR MGD; MGI:107935; Lxlg1.
DR InterPro: IPR007110; IG-1-like.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003591; LRR_Typ.
DR Pfam; PF00047; Ig_3.
DR Pfam; PF00560; LRR_14.
DR Pfam; PF01463; LRRCT_1.
DR Pfam; PF01462; LRRNT_1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SMO0408; IGC2_3.
DR SMART; SMO0082; LRRCT_1.
DR SMART; SMO0013; LRRNT_1.
DR SMART; SMO0369; LRR_Typ_4.
DR PROSITE; PS50835; IG-LIKE; 3.
KM Immunoglobulin domain.
SQ SEQUENCE 1091 AA; 119283 MW; A13D0866CE4C203D CRC64;

Query Match      9.1%; Score 120; DB 11; Length 1091;
Best Local Similarity 22.3%; Pred No. 0.15;
Matches 60; Conservative 40; Mismatches 103; Indels 66; Gaps 10;

OY 14 LQALPPATQGNKRVLGKGGDTVELTCTASQKSAIQFHWKNSNOIKILNGQSGFLT 73
DB 595 LTVNVLPSTFKI PHDIAIRGTGTARLECAATGCHNPQIAWQKDG-----IDFP 643

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OY 74 SKLNRADSRSLNMQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLVFGILTANSPTHL 133
DB 644 A-----ARERRMHWPPDDVVFITVDVKIDMGVSTCAONASGV-----SANATLTV 691
OY 134 LQGSGLTTLTES---PRGSSPSVQCR-----SPRGKNIQGSKTL----- 170
DB 692 LETSLAVPLEDRVVTYGETVAFQCKATGSPRITLWKGGRPLSLTERHHFTPGNQLV 751
OY 171 VSQLELODSGTWCTCTVLONQKKEFKIDIVPRA-SALPAPPTGSLPDPOTASALPDPRA 229
DB 752 VQNMWIDAGRYTCE-MSNPGLTE-----FAHSQSLIIFTPGCRKRDGTGVGIF----- 798
OY 230 ASALPAAVLSFLGLGAGVACVLARTR 258
DB 799 -----TIAVCSITVLSLWVWCITTYOR 821

RESULT 64
ID O97394 PRELIMINARY; PRT; 2222 AA.
AC O97394;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SIDEKICK protein (CGS227-PA) (CGS227-PB).
GN SDK OR BCDNA.LD22322 OR CGS227.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Nguyen D.N.T., Liu Y., Litsky M.L., Reinke R.;
RT "Sidekick, a member of the immunoglobulin superfamily, is required for
RT pattern formation in the Drosophila eye."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

(2)
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abail J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Houston D., Houston K.A., Howland T.J., Wei M.H., Ibsen C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA LaRoche P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spleer E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtk R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

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RA Williams S.M., Woodger, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 Ra Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celisner S.E.,  
 RA Champ M.E., Drysdale R.A., Emmert D., Fries E., de Grey A.D.N.J.,  
 RA Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,  
 RA Russo S., Searle S.M.J., Smith E., Shu S., Smutnak F., Richter J.,  
 RA Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,  
 RA Lewis S.E.;  
 RT "Annotation of *Drosophila melanogaster* genome";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Flybase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Flybase;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U88578; AAD09632.1; -  
 DR EMBL; AE003418; AAF4541.3; -  
 DR PIR; T13924; T13924.  
 DR HSP; P56276; T1K.  
 DR Flybase; FB00021764; sdk.  
 DR InterPro; IPR003962; FntII subd.  
 DR InterPro; IPR003961; FntIII.  
 DR InterPro; IPR008957; FntIII-like.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR Pfam; PF000041; fn3; 13.  
 DR Pfam; PF000047; ig; 5.  
 DR PRINTS; PR00014; FNTYPEIIT.  
 DR SMART; SM00060; FN3; 13.  
 DR SMART; SM00408; IGC2; 4.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 KW Immunoglobulin domain; Repeat.  
 SQ SEQUENCE 2222 AA; 246174 MW; 18853CCAF98DB2 CRC64;

Query Match 9.1%; Score 120; DB 5; Length 2222;  
 Best Local Similarity 24.0%; Pred. No. 0.39;  
 Matches 54; Conservative 30; Mismatches 85; Indels 56; Gaps 11;

DY 26 NKVILGKKGDTVELTCTASQKSIQFPMKNSNQIKILGNGSFLTKGPKSLNDRADRS 85  
 DB 463 NVTLADGDATISGRAVSPNPNTWTWNETQVLDI-----SSRVQ 503  
 QY 86 LMDGNEPLIKNIKIEDSDTYIC-----EVEDQKEVOLLVFGILT-----ANSPTHLIQG 137  
 DB 504 ILSEGD--LISNIRSDAPLYICVRANENGSAEAVALSVLTQIIQPPVDTVILG- 560  
 QY 138 SLVTLSPGSSPSV-----QCRSPKGN-----IQGKTLVSQLELDSDGTWT 183  
 DB 561 -LTAATLQCKVSSDPSVFNIDVREGQSTPISNSQRIQVADQLRIQAVRASDVGSVA 619  
 QY 184 CTVAQ---NKKVFEKIDIVRAALPAPPTG---SALPDPQTSS 222  
 DB 620 CVVTSFGNETRAA-RLSVLT---ELPPPSNVKVERLPEPQAS 659

RESULT 65  
 O9JLM2 PRELIMINARY; PRT; 311 AA.  
 AC O9JLM2;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE NK cell receptor 2B4;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20260988; PubMed=10803843;  
 RA Kumaresan P.R., Stepp S.E., Bennett M., Kumar V., Mathew P.A.;  
 RT "Molecular cloning of transmembrane and soluble forms of a novel rat  
 natural killer cell receptor related to 2B4.";  
 RL Immunogenetics 51:306-313(2000).  
 DR EMBL; AF156989; AAF71162.1; -  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-1like.  
 DR SMART; SM00409; IG; 1.  
 KW Receptor.  
 SQ SEQUENCE 311 AA; 35300 MW; 5A527D22D2565772 CRC64;

Query Match 9.1%; Score 119.5; DB 11; Length 311;  
 Best Local Similarity 22.4%; Pred. No. 0.033;  
 Matches 65; Conservative 43; Mismatches 95; Indels 87; Gaps 14;

DY 12 LVTLALPLPATGQ-----NKVILGKKGDTVELTCTASQKSIQFPMKNSNQIKILGNG 65  
 DB 6 VLTLPLLRHQGDQDCADSSSEVLGSKPRLRPSNIQAKHVSIEWK-----KTHQ 60  
 QY 66 GSEFLTKGPKSLN-DRADRSRL-----MDQNEPLIKNIKIEDSDTYICEVDQK- 115  
 DB 61 -----QTPQIVWDTDNGNFMNCCSDIYGFESENFALSIKAKLNDSGHYLLEITNG 115  
 QY 116 ----BEVQLLVGLTNSDTHL-LQGSILTLTSPGSSPSVQCSPPGKNI-----OG 165  
 DB 116 IVCTKNFQMLIPDPV--ETPHLTVOG-----TLNANGTQSLSCFVPXDQNVSYALYRG 168  
 QY 166 GKTLG-----VSQLELDSDGTCTCTVQNKQKVEFIDIVPRASALPAPPTGSALPD 217  
 DB 169 SMILSNQRYGTWENTDASSLHTYCNVSN-----KAS----- 202  
 QY 218 POTASALPPPPAASALPALAVISPLGLGLVA-----CYLART 258  
 DB 203 -WANHTLTSPQSQSVSKENVLPFWVSIGILVYKFGAIDGCVWNRKR 251

RESULT 66  
 O9M6V2 PRELIMINARY; PRT; 352 AA.  
 ID O9M6V2;  
 AC O9M6V2;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Neurotactin-L.  
 GN NTNA-L.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Brumendorf T.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=99264333; PubMed=10330412;  
 RA Marg A., Strim P., Spaltmann F., Plagge A., Kauselmann G., Buck F.,  
 RA Rachtjen F.G., Brumendorf T.;  
 RT "Neurotactin, A novel neurite outgrowth-promoting Ig-1like protein  
 that interacts with CBP-1 and LAMP.";  
 RL J. Cell Biol. 145:865-876(1999).

DR EMBL: AJ132999; CAB44446.1; -  
DR InterPro: IPR007110; IG\_1like.  
DR InterPro: IPR003598; IG\_c2.  
DR Pfam: PF00047; Ig\_3.  
DR SMART: SM00408; IGc2; 2.  
DR PROSITE: PS50835; IG\_LIKE; 3.  
DR Immunoglobulin domain.  
KW SEQUENCE 352 AA; 37944 MW; B0FA99F295FD8FA0 CRC64;

Query Match 9.0%; Score 119; DB 13; Length 352;  
Best Local Similarity 22.1%; Pred. No. 0.042;

Matches 51; Conservative 40; Mismatches 90; Indels 50; Gaps 10;

QY 20 PAATGNKVVGLGKGDVVELTCTASQKKSIOFHKNSNOIKILGNQSFLLTKGPKLNDR 79  
DB 39 PGAAADSLV--RKDDTVLRCYLEDGAS-KGAMLNRSIIIFAG-----SDK 82  
QY 80 --ADSRSL--WDQGNFPLIIKNLKIEDSDTYICEVDQKE-----EVQLVPEGL 125  
DB 83 WSDPRVSIATANRRREYSLQIDVDVTDGPTGCVQGHPTMQVHLTVQVSPKIFRI 142  
QY 126 TANSPTHLLOQSLLTLIESPPGSSPSVQCR--SPRGKNIQGGKTLVSQLELQDSGTWT 183  
DB 143 --SSDIVNEGSNVTLVCLATGKPEPSISWRHISPSAKPFESGQYLDIYGITRDQAGEYE 200  
QY 184 CTV-----LONOKKVEFKIDIVPRASALPAPPT-----GSALPDP 218  
DB 201 CSAENDSVDPVKVKKVTVNFAPTTQELKSSGVMLGNGLIRCBGAVPAP 251

## RESULT 67

044924 PRELIMINARY; PRT; 1395 AA.

AC 044924  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE ROUNDABOUT 1.  
GN ROBO OR ROBO1 OR CG13521.  
OS Drosophila melanogaster (Fruit Fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
[1]

RA SEQUENCE FROM N.A.  
RX MEDLINE=98117249; PubMed=9458045;  
RA Kild T., Brose K., Mitchell K.J., Felter R.D., Tessier-Lavigne M.,  
RA Goodman C.S., Tear G.;  
RT "Roundabout controls axon crossing of the CNS midline and defines a  
RT novel subfamily of evolutionarily conserved guidance receptors.";  
RL Cell 92:205-215(1998).

DR EMBL: AF040989; AAC38849.1; -  
DR HSPSP; P56276; 1TLK.  
DR FLYBase: FBgn0005631; robo.  
DR GO: GO:0005886; C:plasma membrane; IDA.  
DR GO: GO:0007411; P:axon guidance; IMP.  
DR InterPro: IPR003962; FNIII\_sudd.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR008957; FN\_III-like.  
DR InterPro: IPR007110; IG\_1like.  
DR InterPro: IPR003598; IG\_c2.  
DR Pfam: PF00041; fn3; 3.  
DR Pfam: PF00047; Ig; 5.  
DR PRINTS: PR00014; FNTYPEIII.  
DR SMART: SM00060; FN3; 3.  
DR SMART: SM00408; IGc2; 5.  
DR PROSITE: PS50835; IG\_LIKE; 5.  
KW Immunoglobulin domain; Repeat.  
SQ SEQUENCE 1395 AA; 151778 MW; B820E234A5218983 CRC64;

Query Match 9.0%; Score 119; DB 5; Length 1395;  
Best Local Similarity 25.8%; Pred. No. 0.26;

Matches 59; Conservative 24; Mismatches 94; Indels 52; Gaps 9;

QY 26 NKVVLGKKGDVVELTCTASQKKSIOFHKNSNOIKILGNQSFLLTKGPKLNDADR 85  
DB 353 NKKV-GLNG-VVOLPCNAGNPPSVFWTK-----EGVSTLMFPNSSHGR 395  
QY 86 LMDQGNFPLIIKNLKIEDSDTYICEVDQKEVQLVFGLLTANSDTH---LLOQSLLTLT 142  
DB 396 QYVADGTLQITTDVROEDDEGYVCSAFSVDSITRVFLQVSSVDERPPPIIQIGRANQT 455  
QY 143 LESPSSGSSPSVQCR--SPRGK-----NIQGGKTLVSQLELQDSGTWT 183  
DB 456 L--PKGSVAATLPCGATGNPSPRIKPFHDGAVQAGNRYSTIIQSSSLRVDDLQSDSGTYT 513  
QY 184 CTVLQONKKVEFKIDIVPRASALPAPPTGSA---LDPQTASALPDP 228  
DB 514 CTASGERGETSW-----AATLVKRGSTSLHRAADPSTYPAPPGTP 555

## RESULT 68

08AW79 PRELIMINARY; PRT; 276 AA.

AC 08AW79  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE SI.dz125723.8.1 (Novel immune-type receptor 1.8, variant 1)  
DE (Fragment).  
GN Nitrl.8.  
OS Brachydanio rerio (zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
[1]  
RA SEQUENCE FROM N.A.  
RX Garner P.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL591405; CAD58990.1; -  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR007110; IG\_1like.  
DR Pfam: PF00047; Ig; 2.  
DR SMART: SM00409; IG\_2.  
DR PROSITE: PS50835; IG\_LIKE; 2.  
KW Receptor.  
FT NON TER  
SQ SEQUENCE 276 AA; 30650 MW; 13CAB6090CEC660 CRC64;

Query Match 9.0%; Score 118.5; DB 13; Length 276;  
Best Local Similarity 24.3%; Pred. No. 0.034;  
Matches 53; Conservative 26; Mismatches 72; Indels 67; Gaps 9;

QY 24 QGNKVVGLGKGDVVELTCTASQKKSIOFHKNSNOIKILGNQSFLLTKGPKLNDADR 73  
DB 21 QENNVKLVQAGEDVNLCTFSPNMQLSTAMFKATADGKTLQIYFN--LFTTKSPIMNNV 78  
QY 74 SKLNDRASSRRSLMDQGNFPLIIKNLKIEDSDTYICEVDQKEVQLVFG-----T 126  
DB 79 EKQND-----VNVIIIEGYFNLITLKTNPDSATYYCV-----SYEALIGMGLSRLIVRD 130  
QY 127 ANSDTHLLOQSLLTLIESPPGSSPSVQCR-----LSDVSOLELQDSGTWTCTV 155  
DB 131 AATDRNTLTLQSLDITVD--PGDSVNLQCSIPTFESGAGHSIYFKQSGDSGVLVYTKG 188  
QY 156 -RSPRGNIQGGKTLVSQLELQDSGTWTCTV 186  
DB 189 ERNGRCNKAASSETQSCVYSLHKNINISRSPTGIYCAV 226

RESULT 69  
08AW80 PRELIMINARY; PRT; 278 AA.  
ID 08AW80



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Oy 76 LNDNRASRLMDGNPLLIKLNKIEDSDTYICEVEDOKKEVOLLVFGTA----- 127
Db 90 LMKR-----DISLQIONVNTVDGPTTCSVQIQHPRTQVH-LTVQVPPKIYD 137
Oy 128 -NSDTHLLQGSGLTTLTSPSSPSVOCR--SPRKNIQGGKTLVSQLELDOSGWTWC 184
Db 138 ISNDWTINEGNTVTLTCLATGKPEPVIWMHISPAKFPENGQYLDIGITRDQAGEVEC 197
Oy 185 TV-----LQNKQVEFKDIYPRASALAPPF-----GSAIDP 218
Db 198 SAENDVSPDYKVRVIVNFAPTIOEIKGTVTPGSRGLRCEGAGVPP 247

RESULT 72
Oy 09VP08 PRELIMINARY; PRT; 403 AA.
AC 09VP08;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CG166 protein.
GN CG166.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champ M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Bau A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Nays A.D., Dew I., Dietz S.M., Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fowler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glaeser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C., Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Klamel B.E., Kodira C.D., Kraft C., Kravitz S., Lang D., Lai Z., Lakso P., Lei Y., Levtitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M., Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shu B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhao G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

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RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busan M.A., Carlson J.W., Center A., Champ M., Davenport L.B., Dietz S.M., Dodson K., Dorey V., Dou P.L.E., Doyle C., Dresnek D., Fartan D., Ferreira S., Frise E., Galle R.F., Gary N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hootin D., Howland T.J., Ibegwan C., Jaitani M., Kruse D., Li P., Maltel B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C.A., Nelson K.A., Nuno J., Pacle J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanavong S., Peltman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Miara S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutnack F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003595; AF51754.2;
DR FlyBase; FBgn0037107; CG166.
DR InterPro; IPR001064; CysTallin.
DR InterPro; IPR008957; FN-III-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IG_3.
DR SMART; SM00408; IGc2_3.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 403 AA; 45747 MW; 429C1039F539F76D CRC64;

Query Match 9.0%; Score 118; DB 5; Length 403;
Beet Local Similarity 23.9%; Pred. No. 0.062;
Matches 45; Conservative 34; Mismatches 75; Indels 34; Gaps 9;

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Db 33 KVIY---GTEILPCKQKNGSFTVLMRKSS-----SVLTAGHLKIT--RDQFKI 78

Oy 87 WDGNPFLIKLNKIEDSDTYICEVEDOKE-----VOLLV---FGLTNSDTHLLQGO 137
Db 79 --VDGNYLQINGVTQDAGDYICQLGQENRDQVHTVEILVPTLRALPHNGVGTARKS 136

Oy 138 SLTTLTSPSSPSV-----QSRPKNIQGGKTLVSQLELDOSGWTWCVLONQ 191
Db 137 TVTLECAASNPVFTTFWFKDVFSGP--THLSDSTLTILENDRHAGTYQCSA-DNGV 193

Oy 192 KVEFKIDI 199
Db 194 KDRVSMDI 201

RESULT 73
Oy 09D221 PRELIMINARY; PRT; 577 AA.
AC 09D221;

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DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE 9130012D09Rik protein.
GN 9130012D09Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RC STRAIN=FVB/N; TISSUE=Cecum;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gisi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirnl L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guarnieri S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayaishi Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
DR EMBL; AK018613; BAB3107.1; -
DR MGD; MGI:1918851; 9130012D09Rik.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; 1.
KV Immunoglobulin domain
SQ SEQUENCE 577 AA; 63444 MW; C3470C7B60FB8B2B CRC64;

Query Match 9.0%; Score 118; DB 11; Length 577;
Best Local Similarity 22.5%; Pred. No. 0.099;
Matches 60; Conservative 42; Mismatches 91; Indels 74; Gaps 12;

QY 13 VLQALLPATQGN---KVLGKKGDTVELTCTASQKSIQPFMKNSNQIKILNGSGF 68
DB 227 VVKQVLEKVTAPNIEPFTLALVENATSVTLCTKSHQR-VGVNM-----F 271
QY 69 LTKGPEKLNDRADRSRLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEVOLVFGITAN 128
DB 272 LKQGPLRPSPDRL---TLSSQ-NRTLTIHGLQRDDIGPECEVNMNSQARSVPKLTIN 326
QY 129 ---SDTHLQG--QSLTLTLESPGSSPSVQCRS-----PRGNKIQGKTLV 171
DB 327 YGPDQVEITQGPASGVSTIEAMLNSSLTLYCRADSIPEARQWTHHESSKVLDDGELSI 386
QY 172 SQLELDSDSGTWCTVQLQNKQKVEFKIDIVPRASALPAPPGSALPDQPTASAL---PDP 228
DB 387 EALRQEHQGIYSTCTSSND-----VTGLA---RSASVLMVVGQLQ 422
QY 229 AASALPALA-----VISFLGLGLG 249
DB 423 SSSMSFPAIAGIVIGIIVATAIGLG 449

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ID 080Y42 PRELIMINARY; PRT; 577 AA.
AC 080Y42;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE 9130012D09Rik protein.
GN 9130012D09Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.L., Feilings E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abrahams R.D., Whillans S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Skalko J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywicki M.I., Gilmak U., Smaluk D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX EMBL; BC049361; AAH49361.1; -
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049361; AAH49361.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGC2; 4.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; 1.
KV
SQ SEQUENCE 577 AA; 63426 MW; EF52B146A50EB871 CRC64;

Query Match 9.0%; Score 118; DB 11; Length 577;
Best Local Similarity 22.5%; Pred. No. 0.099;
Matches 60; Conservative 42; Mismatches 91; Indels 74; Gaps 12;

QY 13 VLQALLPATQGN---KVLGKKGDTVELTCTASQKSIQPFMKNSNQIKILNGSGF 68
DB 227 VVKQVLEKVTAPNIEPFTLALVENATSVTLCTKSHQR-VGVNM-----F 271
QY 69 LTKGPEKLNDRADRSRLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEVOLVFGITAN 128
DB 272 LKQGPLRPSPDRL---TLSSQ-NRTLTIHGLQRDDIGPECEVNMNSQARSVPKLTIN 326
QY 129 ---SDTHLQG--QSLTLTLESPGSSPSVQCRS-----PRGNKIQGKTLV 171
DB 327 YGPDQVEITQGPASGVSTIEAMLNSSLTLYCRADSIPEARQWTHHESSKVLDDGELSI 386
QY 172 SQLELDSDSGTWCTVQLQNKQKVEFKIDIVPRASALPAPPGSALPDQPTASAL---PDP 228
DB 387 EALRQEHQGIYSTCTSSND-----VTGLA---RSASVLMVVGQLQ 422
QY 229 AASALPALA-----VISFLGLGLG 249

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Db 423 SSSMPCALAGIVIGILVIALAIGLG 449

RESULT 75  
 ID Q9W213 PRELIMINARY; PRT; 1395 AA.  
 AC Q9W213;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE CG13521 protein.  
 GN ROBO OR CG13521.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 CC NCBI\_TaxID=7227;  
 RN [1]  
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 RC STRAIN=Berkley;  
 RC MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Baau A., Bakendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Bokoyva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Butts K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jajal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Klumel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Amanatides P.G., Brandon R.C., Rogers Y., An H., Baldwin D.,  
 RA Batzon J., Beeson K.Y., Buam D.A., Carlson J.W., Center A.,  
 RA Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V.,  
 RA Doup L.E., Doyle C., Dresnek D., Farfan D., Ferritara S., Frise E.,  
 RA Galle R.F., Garg N.S., George R.A., Gonzalez F., Houck J.,  
 RA Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jajal M.,  
 RA Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M.,  
 RA Murphy B., Nelson C., Nelson K.A., Nuno J., Pacle J., Paragas V.,  
 RA Park S., Patel S., Pfeiffer B., Phouanavong S., Pittman G.S.,  
 RA Puri V., Richards S., Scheeler F., Stapleton M., Strong R.,  
 RA Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S.,  
 RA Smith H.O., Venter J.C., Rubin G.M.;

RT "Sequencing of Drosophila melanogaster genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.

RA Miya S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,  
 RA Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,  
 RA Harris N.L., Krommiller B., Marshall B., Milburn G.H., Richter J.,  
 RA Russo S., Searle S.W.D., Smith E., Shu S., Smutnjak F.,  
 RA Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Mungall C.J., Lewis S.E.;  
 RT "Annotation of Drosophila melanogaster genome.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AE003458; AAM71113.1; -;  
 DR HSSP; P56276; ITLK.  
 DR FlyBase; FBgn005631; robo.  
 DR GO; GO:0005886; C:plasma membrane; IDA.  
 DR GO; GO:0007411; P:axon guidance; IMP.  
 DR InterPro; IPR003962; PiliI subd.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR007110; IG\_III-like.  
 DR Pfam; PF00041; fn3; 3.  
 DR Pfam; PF00047; Ig; 5.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR Repeat.  
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 Best Local Similarity 25.3%; Pred. No. 0.31; Indels 52; Gaps 10;  
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 QY 26 NKVVLGKKGPVETLTASQKSIQFHKNSNQIKILGNOSPLTKPSKLNDRADSRRS 85  
 DB 353 NKKV-LGNG-VQGLPCASGNPPSVWTEGVSTLM-----FNNSHGHQVAAVG--- 402  
 QY 86 LMDQGNPPLIKKIKEDSTTYICEVDQKEVQLVFGTANSDDH---LLQGOSLTLT 142  
 DB 403 -----TLITVROQDEGVYVCSAFVSVDSTVRFVLVSSIDERPPIIQIGPANOT 455  
 QY 143 LESPPGSSPVSQCR-----SPRCK-----NIQGGKTLVSQLELDGSGTWT 183  
 DB 456 L-PKGSVATLPCCATNPSPRIKMFHDGAAVQAGNRYSLIIGSSLVVDLQSDSGTIT 513  
 QY 184 CTVLQNKQKVEFKIDIVPRASALPAPPTGSA---LPDPOTASALPDP 228  
 DB 514 CTASGGERGERSW-----AATLVEKRGSTSLHRADPSTYPAPPTGP 555  
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 AC Q8IRV9;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE CG7981-PC.  
 GN TROL OR EG:BACR2583.11 OR CG7981.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 CC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,



RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Arril J.F., Agapayni A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
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RA Beeson K.Y., Benoe P.V., Berman B.P., Bhargava P.D., Bolshakov S.,  
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hock J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeagwa C.,  
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Kechum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
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RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paalel J.M.,  
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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,  
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RT The genome sequence of *Drosophila melanogaster*. ;  
PL Science 287:2195-2195(2000) .

RP SEQUENCE FROM N.A.  
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RA Williams S.M., Zavari J.S., Smith H.O., Venter J.C., Rubin G.M.,  
RT "Sequencing of *Drosophila melanogaster* genome."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBD databases.  
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RA Misra S., Crosby W.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
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RT "Annotation of *Drosophila melanogaster* genome."  
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RA FlyBase;  
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DR EMBL; AEO03424; AAN09077.1; -  
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DR GO; GO:0005198; F:structural molecule activity; IEA.

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 Science 287:2185-2195(2000).  
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 Celinker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 Barton J., An H., Baldwin D., Barton J., Beeson K.Y., Buesam D.A.,  
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 "Sequencing of *Drosophila melanogaster* genome.";  
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [3]  
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 Maier S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
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 Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
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 Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 "Annotation of *Drosophila melanogaster* genome.";  
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 SEQUENCE FROM N.A.

Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [5]  
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 FlyBase;  
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 EMBL; AE003424; AAF45786.3; -  
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 GO; GO:0005198; F:structural molecule activity; IEA.  
 GO; GO:0006306; P:DNA methylation; IEA.  
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 InterPro; IPR007742; EGF\_2.  
 InterPro; IPR006209; EGF\_1like.  
 InterPro; IPR003599; Ig\_1like.  
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 InterPro; IPR003598; Ig\_c2.  
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 InterPro; IPR002049; laminin\_EGF.  
 InterPro; IPR001791; laminin\_G.  
 InterPro; IPR002172; LDL\_receptor\_A.  
 InterPro; IPR000504; RNA\_rec\_mot.  
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 Pfam; PF00053; laminin\_EGF\_2.  
 Pfam; PF00054; laminin\_G\_3.  
 Pfam; PF00057; ldl\_recept\_a; 23.  
 PRINTS; PR00261; LDLRECEPTOR.  
 SMART; SM00180; EGF\_lam; 9.  
 SMART; SM00409; IG\_12.  
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 SMART; SM00281; lamB; 3.  
 SMART; SM00282; lamG; 3.  
 SMART; SM00192; LDLA; 23.  
 PROSITE; PS00094; C5\_MTASE\_1; 1.  
 PROSITE; PS00022; EGF\_1; 10.  
 PROSITE; PS01186; EGF\_2; 6.  
 PROSITE; PS50835; IG\_LIKE; 11.  
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 PROSITE; PS50025; LAM\_G\_DOMAIN; 3.  
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 Db 3193 REGENIDLOCTVTDQYVRAQDNVERFWFRDD-----RRLPNMATDQ-- 3227  
 Oy 86 LMDQGNFPLIIKKILKIDSDTYICEVD-----QKEVQLLVFGLT---NSDTHL-- 133  
 Db 3238 -----ILVITNLRPDPADGRYICNSYDVDRGQQLPEVSIDLQVLTFTPPNSPIYLPQ 3290  
 Oy 134 --LQGSGLTLLEBP-----PGSSPSVQCS-----PRKNT-OGGKTL 169  
 Db 3291 LPAASRYSLKLDQSSNLRAGSTDVCEYSDDTYTVDVWERSDGAFLNNVRQVGNRL 3350  
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 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Perlecan (CG7981-PD).  
 GN TROLO OR EG:BACR25B3.11 OR CG7981.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NBI\_taxid=7227;  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Voigt A.;  
 RT "perlecan participates in proliferation activation of quiescent  
 RT Drosophila neuroblasts";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
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 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
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 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
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 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
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 RT "Sequencing of Drosophila melanogaster genome";

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 RA Seale S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
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 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
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 DR InterPro; IPR001525; C5\_DNA\_meth.  
 DR InterPro; IPR008985; ConA\_like\_1ec\_g1.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR003599; Ig\_1like.  
 DR InterPro; IPR007110; Ig\_1like.  
 DR InterPro; IPR003598; Ig\_G2.  
 DR InterPro; IPR000034; Laminin\_B.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR002172; LDL\_receptor\_A.  
 DR InterPro; IPR000504; RNA\_rec\_mot.  
 DR Pfam; PF00067; 1g\_13.  
 DR Pfam; PF00052; Laminin\_B\_3.  
 DR Pfam; PF00053; Laminin\_EGF\_2.  
 DR Pfam; PF00054; Laminin\_G\_3.  
 DR Pfam; PF00057; 1dl\_recept\_a; 23.  
 DR PRINTS; PR00261; LDLRECEPTOR.  
 DR ProDom; PD003031; Laminin\_B\_3.  
 DR SMART; SM00180; EGF\_Lam; 8.  
 DR SMART; SM00409; IG\_13.  
 DR SMART; SM00408; IGC2; 13.  
 DR SMART; SM00281; Lamb; 3.  
 DR SMART; SM00282; Lamg; 3.  
 DR SMART; SM00192; LDLa; 23.  
 DR PROSITE; PS00094; C5\_WTASE\_1; 1.  
 DR PROSITE; PS00022; EGF\_1; 10.  
 DR PROSITE; PS01186; EGF\_2; 6.  
 DR PROSITE; PS00835; IG\_Like; 12.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 7.  
 DR PROSITE; PS00025; LAM\_G\_DOMAIN; 3.  
 DR PROSITE; PS01209; LDLRA\_1; 20.  
 DR PROSITE; PS00068; LDLRA\_2; 23.  
 DR PROSITE; PS00030; RRM\_RNP\_1; 1..  
 KM Immunoglobulin domain.  
 SQ SEQUENCE 4223 AA; 466919 MW; 31D7C2B5C9B1D2E0 CRC64;  
 Query Match 9.0%; Score 118; DB 5; Length 4223;  
 Best Local Similarity 23.1%; Pred. No. 1.3; 55; Indels 64; Gaps 9;  
 Matches 45; Conservative 31; Mismatches  
 Qy 32 KKSDYELTCTASQ-----KSIQPHWKNNSQIKILGNQGSFLTGPSKLNDRADSRRS 85  
 Db 3237 RSENIQLQCTVVDYGVRAQDVERNMRPD-----RRPLNNKRTISQ-- 3281  
 Qy 86 LMDQGNFPLIKNLKIEDSDTYICEVED-----QKEEVOLVFGLTAA---NSDTHL--- 133

Db 3282 -----ILVLTNLRPEDAGRYICNSYDVDRGQQLPEVSIQLQVLTATPPNPSPYLPQP 3334  
 QY 134 --LOGQSLTTLRES-----PGSSPSVQCRS-----PRGKNT-QGCKTL 169  
 Db 3335 LPASRDYSLKLDQSSNLRAGESTDEVCSSDDTYTDVWERSDGAFLSNVROVGNRL 3394  
 QY 170 SVSOLEQDSGTWTC 184  
 Db 3395 VISNVSPSDAGNYVC 3409

RESULT 79  
 Q23550 PRELIMINARY; PRT: 6831 AA.  
 ID Q23550 Q23020, Q27232; 01. Created)  
 AC Q23550, Q23020, Q27232; 01. Created)  
 DT 01-NOV-1996 (TREMBLrel. 01. Created)  
 DT 01-NOV-1998 (TREMBLrel. 08. Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25. Last annotation update)  
 DE UNC-22 protein.  
 GN UNC-22 OR ZK617.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxId=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA White S., Harris B.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 784-6831 FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=90044042; PubMed=2812002;  
 RA Benian G.M., Kilt J.E., Neckelmann N., Moerman D.G., Waterson R.H.;  
 RT "Sequence of an unusually large protein implicated in regulation of  
 RT myosin activity in C. elegans."  
 RL Nature 342:45-50(1989).  
 RN [3]  
 RP SEQUENCE OF 784-6831 FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=9387664; PubMed=8397135;  
 RA Benian G.M., L'Hernault S.W., Morris M.E.;  
 RT "Additional sequence complexity in the muscle gene, unc-22, and its  
 RT encoded protein, twitchin, of Caenorhabditis elegans."  
 RL Genetics 134:1097-1104(1993).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=a;  
 CC IsoId=Q23550-1; Sequence=Displayed;  
 CC Note=No experimental confirmation available;  
 CC Name=b;  
 CC IsoId=Q23551-1; Sequence=External;  
 CC Note=No experimental confirmation available;  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; Z73897; CA98064.1; -  
 DR EMBL; Z73899; CA98081.1; JOINED.  
 DR EMBL; Z73897; CA98081.1; JOINED.  
 DR EMBL; X15423; CA93463.1; -  
 DR PIR; A88852; A88852.  
 DR PIR; S57242; S57242.  
 DR HSP; O63450; 1A06.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0004812; F:tRNA ligase activity; IEA.  
 DR GO; GO:0006418; P:amino acid activation; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR003962; FNIII\_sabd.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR007110; IG\_III-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_kin\_AS.  
 DR InterPro; IPR001412; tRNA-synt\_1.  
 DR Pfam; PF00041; fn3; 31.  
 DR Pfam; PF00047; ig; 21.  
 DR Pfam; PF00069; kinase; 1.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PRODOM; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00060; FN3; 27.  
 DR SMART; SM00408; IGc2; 6.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_I; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 21.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR Hypothetical protein; ATP-binding; Alternative splicing;  
 KW Immunoglobulin domain; Kinase; Repeat;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 6831 AA; 752596 MW; 6C4DE032963A52E1 CRC64;

Query Match 9.0%; Score 118; DB 5; Length 6831;  
 Best Local Similarity 23.3%; Pred. No. 2.5;  
 Matches 58; Conservative 36; Mismatches 87; Indels 68; Gaps 12;

QY 8 RHLLVQLALPAPATGKAVYLGKGDYELTCTAQSQSIQPHWKNQIKILGNQGS 67  
 Db RHFFV-----PKSQ--RV--NESDLTLETVDVNDKAEVVMHDKRIDIDGVK-- 1032  
 QY 68 FLTKGPSKLNDRADRSRLMDQGNFPLIKLKTIEDSDTYICEVDEQKEEYQLLVFG-- 124  
 Db -----KRVSSNRKR-----LIINGARIEDGEYKCTKDRPTAQLIVDAKNK 1077  
 QY 125 -LTANSDTHLLOGSLTTLTSPGSSPSVQCRSPRKNTQ--GK-----TLS 170  
 Db 1078 FIVALKOTEVIEKQDVLTMCQTKOTKTPGAIWFRV--GKQISSMVGKFEETQSRNGTTLK 1135  
 QY 171 VSQLELDS-----GTWCTYVLQND-----KQVEFKDIYPRASALPAFP 210  
 Db 1136 IGIENKAEADVVEIDQGLRGSCNVTLAEKRPILMKPKIEAKAG-EPCVAVKVPFOI 1194  
 QY 211 TGSALPDPQ 219  
 Db 1195 KGTGRGDPK 1203

RESULT 80  
 Q23551 PRELIMINARY; PRT: 7158 AA.  
 ID Q23551  
 AC Q23551;  
 DT 01-NOV-1996 (TREMBLrel. 01. Created)  
 DT 01-JUN-2003 (TREMBLrel. 24. Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25. Last annotation update)  
 DE Hypothetical protein ZK617.1b (C. elegans UNC-22 protein)  
 DE (Corresponding sequence ZK617.1b).  
 GN ZK617.1b OR UNC-22.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxId=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA White S.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

```

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Briscot N2;
RA Harris B.R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z73897; CA98065.2; -
DR EMBL; Z73899; CA98065.2; JOINED.
DR EMBL; Z73897; CA98082.2; JOINED.
DR EMBL; Z73899; CA98082.2; -
DR PIR; T27935; T27935.
DR PIR; 1K0A; 30-APR-99.
DR PDB; 1WIT; 23-DEC-96.
DR PDB; 1WIT; 23-DEC-96.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:Protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:Protein-tyrosine kinase activity; IEA.
DR GO; GO:0004812; F:RNA ligase activity; IEA.
DR GO; GO:0006418; P:amino acid activation; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR003962; FNII subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR001412; CRNA-synt_1.
DR InterPro; IPR01245; Tyr_kinase.
DR Pfam; PF00047; fn3; 31.
DR Pfam; PF00047; ig; 21.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00014; FNTPETII.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00060; FN3; 32.
DR SMART; SM00409; IG; 30.
DR SMART; SM00408; IGC2; 24.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR PROSITE; PS50835; IG_LIKE; 21.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR HypoProteomic; HYP000001; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 7158 AA; 788947 MW; 561EF9DB13387505 CRC64;

Query Match 9.0%; Score 118; DB 5; Length 7158;
Best Local Similarity 23.3%; Pred. No. 2.7;
Matches 56; Conservative 36; Mismatches 87; Indels 68; Gaps 12;

QY 8 RHLLVLVQLALPPATQGNKRVLGKGGDTVELTCTASQKKSIOFHWNINSQIKLGNQGS 67
DB 1313 RHTEFVV-----PKKSGQ-KV---NESDLATLETDVNDKDAEYVWMHDKRIDIDGVK-- 1359
QY 68 FLTGSPSKLNDRADRSRLMDQGNPFLIKNLKIEDSDTYICEVEDQKEVQVLVFG--- 124
DB 1360 -----FKVSSSNKRR-----LILINGARLEDEGEYKCTTKDRITVAQLIVDAKMK 1404
QY 125 -LTANSDTHLLOGSLTTLTSPGSSPSVQCRSPKKNIO---GK-----TLS 170
DB 1405 FIYALNKTVEYKNDVILMCTQTKTKPIGWFRN--GKQISSMGSGFETQSRNGHTTLK 1462
QY 171 VSQLELQDS-----GTWTCVVLQNO-----KQVEFKIDIVPRASALPAP 210
DB 1463 IGIKENMEADVYIEDQGLRGSQNVTVLEAKRPILNWKPKLEAKAG-EPGVKVPFQI 1521
QY 211 TGSALPPQ 219
DB 1522 KGTGRGDPK 1530

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RESULT 81
ID 002869 PRELIMINARY; PRT; 350 AA.
AC 002869;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CHLAMP, g11-isoform precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=97358596; PubMed=9215692;
RA Brummenhof T., Spaltmann F., Treubert U.;
RT "Cloning and characterization of a neural cell recognition molecule on
RT axons of the retinorectal system and spinal cord."
RL Eur. J. Neurosci. 9:1105-1116(1997).
DR EMBL; Z94719; CAB08114.1; -.
DR PIR; JCS519; JCS519.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR Brain; GPI-anchor; Immunoglobulin domain; signal.
FT SIGNAL 1
FT CHAIN 29 350 CHLAMP, g11-ISOFORM.
SQ SEQUENCE 350 AA; 38656 MW; 0844A892878894D4 CRC64;

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Query Match 8.9%; Score 117; DB 7; Length 350;
Best Local Similarity 22.4%; Pred. No. 0.063;
Matches 55; Conservative 41; Mismatches 93; Indels 56; Gaps 11;

QY 10 LLLVLDLALPPA-----TQGNKRVLGKGGDTVELTCTASQKKSIOFHWNINSQIKI 61
DB 14 LVLLRLCLLPGLPGRVSDPFRGDTNITVRQSDTALILCFVEDRNS-KVAMLNRSGLIF 72
QY 62 LGNQSFLTKGSPSKLNDRAD-SRSLMDQGNPFLIKNLKIEDSDTYICEVEDQ---KE 116
DB 73 AG-----EDKKSIDPRVLEKRSPLF---YSLRIQKVDYDEGSYTSVQGHHPKIS 122
QY 117 EVQVLVFG---LTANSDTHLLOGSLTTLTSPGSSPSVQCR--SPKKNIOGSGKT-L 169
DB 123 QVTLIVQVPPKISNISSDITVNEGSNVTLCMANGRPPEVITWRHLPTGKEFEGESEYL 182
QY 170 SVSQLELQDSGTWTCVVLQ-----NOKVEFKIDIVP-----RAS 204
DB 183 EIIGITREOSGKYECRAANEVASADYKQVRVTVNYPITTESKSNMAATGRQALLCEAS 242
QY 205 ALPAP 209
DB 243 AVPTP 247

RESULT 82
Q9VNP2
ID Q9VNP2 PRELIMINARY; PRT; 811 AA.
AC Q9VNP2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CG8779 protein.
GN NRM OR CG8779.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
[1]

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RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoekne R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chapple M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKlos G.L.G.,  
 RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,  
 RA Borokov D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,  
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hooten D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson M.,  
 RA Mekulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,  
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*";  
 RL Science 287:2185-2195(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Barzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoekne R.A., Hooten D., Howland T.J.,  
 RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,  
 RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phoumanavong S., Peltman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of *Drosophila melanogaster* genome";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Miara S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hrdceky P., Huang Y., Kaminker J.S., Prochownik S.E., Smith C.D.,  
 RA Rudy J.L., Bergman C., Bernier B., Carlson J.W., Celniker S.E.,  
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of *Drosophila melanogaster* genome";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003599; AAF51887.2; -  
 DR FlyBase; FBgn0005629; nrm.  
 DR GO; GO:0005886; C:plasma membrane; IDA.  
 DR InterPro; IPR002086; Aldenhyde\_dehydr.  
 DR InterPro; IPR003599; IG\_1like.  
 DR InterPro; IPR007110; IG\_1like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; IG\_6.  
 DR SMART; SM00409; IG\_5.  
 DR SMART; SM00408; IGC2; 4.  
 DR PROSITE; PS00070; ALDENHYDE\_DEHYDR\_CYS; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 7.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 811 AA; 90442 MW; BAC689EA2C8E23F4 CRC64;  
 Query Match 8.9%; Score 117; DB 5; Length 811;  
 Best Local Similarity 25.0%; Pred. No. 0.19; Mismatches 30; Gaps 9;  
 Matches 48; Conservative 38; Mismatches 76; Indels 30; Gaps 9;  
 Oy 10 LLVLTQALTPAAT-QGNKVVLGKKGDPVELTCTASQKSIQFH-----WKNNOI--KIL 62  
 Db 26 LVVLCLALVDSSTAQVDTTISQGSQSVLPCEVDAEKCKLHSLMMFKGDDRIAMTL 85  
 Oy 63 GNQGSFLTKGSKLNDRAHSRLMDQGNFPLIKLIKEDSDTYICEVEDQKEVQLLV 122  
 Db 86 GD-----SVNTSVNKEFDERVTV-EQNRYLVTKDKLADIEDIYLCDT-----T 128  
 Oy 123 FGLTNSDTHLQGSLLTLESPPGSSPSVQCSPPGKNTGGKTLTSVSLQLEIDSGTW 182  
 Db 129 FFIIEETCDN-FNGYRIELRLVPP--TEVVIIDAKGRDIKNGSV--VGPMSERQSLKA 182  
 Oy 183 TCTVLAQNKVYE 194  
 Db 183 TCTYRNRPPQPE 194  
 RESULT 83  
 Q24273 PRELIMINARY; PRT; 1011 AA.  
 AC Q24273;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE NEURONUSCULIN.  
 GN NRM OR CG8779.  
 OS *Drosophila melanogaster* (fruit fly)  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; *Drosophila*.  
 OC NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=94000831; PubMed=8398154;  
 RX Kania A., Han P.L., Kim Y.T., Belien H.;  
 RT "Neuromusculin, a *Drosophila* gene expressed in peripheral neuronal  
 RT precursors and muscles, encodes a cell adhesion molecule";  
 RL Neuron 11:673-687(1993).  
 RL EMBL; L23146; AAA03750.1; -  
 DR PIR; T13669; T13669.  
 DR FlyBase; FBgn0005629; nrm.  
 DR GO; GO:0005886; C:plasma membrane; IDA.  
 DR InterPro; IPR003599; IG\_1like.  
 DR InterPro; IPR007110; IG\_1like.  
 DR Pfam; PF00047; IG\_8.  
 DR SMART; SM00409; IG\_5.  
 DR PROSITE; PS50835; IG\_LIKE; 9.  
 KW Cell adhesion.  
 SQ SEQUENCE 1011 AA; 113125 MW; APD8A2A015D3AE63 CRC64;

```

Query Match      8.9%; Score 117; DB 5; Length 1011;
Best Local Similarity 25.0%; Pred. No. 0.25; Indels 30; Gaps 9;
Matches 48; Conservative 38; Mismatches 76; Indels 30; Gaps 9;

QY 10 LLLVLTQALLPAAT-QGNKVLGKGDVLTCTASQKSIQPH---MKNSNQI---KIL 62
DB 26 LVLVLICALVDSSTAVQDTTISQGESQSVLPCEVDAEKCKGLHSLNWFQGDRIAMLL 85
QY 63 GNGOSFLTKPSPKLNDRADSRSLMDQGNFLLIKLKIEDSPTYICEVEDQKEVOLV 122
DB 86 GD-----SNVTSYKKEFDERVTY-EQNPRYLVIKDKIADIEDIYICDT-----T 128
QY 123 FGLTANSDTHLQGSQSLTLTLESPPGSSPSVQCRSPRKNIOGKTLVSQLELDPSGT 182
DB 129 FFIPEETCDN-FNGYRIELHVLVP---TEVITLIDAKGRIRKNGSV--VGPWQEROSLKA 182
QY 183 TCTVLQNOQKVE 194
DB 183 TCTVTRNRPQPE 194

RESULT 84
Q7TQ03 PRELIMINARY; PRT; 192 AA.
ID 07TQ03
AC 07TQ03
DT 01-OCT-2003 (Tremblrel..25, Created)
DT 01-OCT-2003 (Tremblrel..25, Last sequence update)
DT 01-OCT-2003 (Tremblrel..25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CS7BL/6J; TISSUE=Blasocycat;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.J.,
RA Rana S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huik S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skaleja U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CS7BL/6J; TISSUE=Blasocycat;
RA Strausberg R.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052651; AAH52651.1; -.
KM Hypothetical protein.
SQ SEQUENCE 192 AA; 20905 MW; E4213FCE00540D7F CRC64;

Query Match      8.8%; Score 116.5; DB 11; Length 192;
Best Local Similarity 29.0%; Pred. No. 0.032; Indels 51; Gaps 8;
Matches 64; Conservative 19; Mismatches 82; Indels 51; Gaps 8;

QY 10 LLLVLTQALLPAATQGNKVLGKGDVLTCTASQKSIQPH---MKNSNQI---KIL 68
DB 6 VLLSTFLLLPAAAGARQEVHGTGDPVLPFCVSPESRIISFVCMGEGCASDTCGTLV 65

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QY 69 LTKGSPKLNDRADSR---RSLMDQGNFLLIKLKIEDSPTYICEVEDQKEVOLV 125
DB 66 WTDG--HRVRYRTSRNRQINSQLLQGNASTLTLEYAESDGLVCCRYE----- 111
QY 126 TANSDFHLQG---QSLTLTLESPPGSSPSVQCRSPRKNIOGKTLVSQLELDPSGT 181
DB 112 -----MKMGDGVQTLTTSIQIQPGSS-----SARKGLAIG--LSIFLLVLVNGT 155
QY 182 WTCTVLQNOQKVEFKIDIVPRASALPAPPTGAL 215
DB 156 LVITNYIIMKK-----RPEPSLVAL 176

RESULT 85
O43608 PRELIMINARY; PRT; 285 AA.
ID O43608
AC O43608
DT 01-JUN-1998 (Tremblrel..06, Created)
DT 01-JUN-1998 (Tremblrel..06, Last sequence update)
DT 01-OCT-2003 (Tremblrel..25, Last annotation update)
DE Roundabout 2 (Fragment).
GN ROBO2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98117249; PubMed=9458045;
RA Kidd T., Brose K., Mitchell K.J., Fetter R.D., Tessier-Lavigne M.,
RA Goodman C.S., Tear G.;
RT "Roundabout controls axon crossing of the CNS midline and defines a
RT novel subfamily of evolutionarily conserved guidance receptors."
RL Cell 92:205-215 (1998).
DR EMBL; AF040991; AAC39576.1; -.
DR GO; GO:0008046; Paxon guidance receptor activity; NAS.
DR GO; GO:0007417; P-centra nervous system development; NAS.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KM Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 285 AA; 30606 MW; 05DF916A3DBA96C6 CRC64;

Query Match      8.8%; Score 116.5; DB 4; Length 285;
Best Local Similarity 22.8%; Pred. No. 0.053; Indels 69; Gaps 13;
Matches 58; Conservative 32; Mismatches 95; Indels 69; Gaps 13;

QY 33 KEDTVLTCTASQKSIQPHMKNSNQIKLNGSFLTKGSPKLNDRADSRSLMDQGNF 92
DB 5 QGRTVTFPCTKGNPOPAVFWQKE-----GSGNLLFPNQOQPN---SRCSVSPTGD- 53
QY 93 PLTIKLIKIEDSPTYICEVEDQKEVOLVFG-LTANSQ---THLQGSQSLTLTLESPPG 148
DB 54 -LTIITNIGSDAGYICQA-----LTVAGSIILAKQLEVTVDLTDRPPILLQGRAN 104
QY 149 SSPSV-----QC-----RSPRKNIOGKTLVSQLELDPSGT 181
DB 105 QTLAVDGTALMKCATGDLPLVISMKEGTFPRGDPRA-TIQEGTLLQIKNIRISPTGT 163
QY 182 WTCTVLQNOQKVEFK-IDIVRA-----SALPAPPTGALPD---PQTASALPD 226
DB 164 YTCVATSSGGEASWSAVLDTESGATISKNYDLSLPGPPSKQVTDVTKNSVTLNQPG 223
QY 227 PPAASALPALAVI 240

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Db 224 TP-CTLPASAVII 235

RESULT 86  
Q9V6C2 PRELIMINARY; PRT; 359 AA.  
ID Q9V6C2  
AC Q9V6C2  
DT 01-MAY-2000 (TrEMBLrel. 13 Created)  
DT 01-MAY-2000 (TrEMBLrel. 13 Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE LAC protein (LJ34460P).  
GN LAC OR CG12369.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
NCBI\_TaxID=7227;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132.  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Bailew R.M., Baau A., Bakendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
RA Bokoy D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
RA Burlis K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iqbalwan C.,  
RA Jaisi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mactel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,  
RA Palazzolo M., Peltan G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champagne M., Chavez C., Doresett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nunoo J., Pacleb J., Parasas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003822; AAF58506.1; -;  
DR EMBL; AY051829; AAK93253.1; -;  
DR HSSP; P56276; ITK.  
DR FlyBase; FBgn0010238; Lac.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR Pfam; PF00047; Ig\_3.  
DR SMART; SM00408; IGC2; 2.  
DR PROSITE; PS50835; Ig-LIKE; 3.  
KW Immunoglobulin domain.  
SQ SEQUENCE 359 AA; 39939 MW; 12F513E2B9C156F4 CRC64;  
Query Match 8.8%; Score 116.5; DB 5; Length 359;  
Best Local Similarity 22.3%; Pred. No. 0.072;  
Matches 47; Conservative 34; Mismatches 87; Indels 43; Gaps 7;  
Db 34 GDTVELCTASQKSIQIFHWKNSNQIKILNGQSFILTKGPKLNDRADRSRLDQGNFP 93  
43 GGVTEPDCSQYAKENVVLFLKTDSDVPLSTGTVLTKSRFSLRYDPNS-----TYK 97  
Qy 94 LIINKLIEDSDTYICE-----VEDQEEVQLVFGLTANSDFLLQGQSITLTLESPPG 148  
Db 98 LQIKDIQETDAGTFCQVIVSTVHKVSAEVLTVSRPPVLSID-----NSTQSVASEG 150  
Qy 149 SSPSVQCRS-----PRKNIGQKTLVSQSLQELQSDSGTWCTVQLON- 189  
Db 151 SEVQMECYAGPYPTITWRRENNALPTDSATYVNTLRKSVKEDRGTYVC-VADNG 209  
Qy 190 -----OKVFEKIDIVRASALPAPPGSAL 215  
Db 210 VSKCDRNINVEVFAP-VITVPRRLQAL 239

RESULT 87  
Q8NCE6 PRELIMINARY; PRT; 570 AA.  
ID Q8NCE6  
AC Q8NCE6  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein FLJ90299.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
RP Isegal T., Oca T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,  
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hiro Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,  
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,  
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;  
RT "NEDO human cDNA sequencing project."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK074780; BAC11205.1; -;  
DR InterPro; IPR003962; FNIII\_subd.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003599; Ig\_III-like.  
DR InterPro; IPR007110; Ig-LIKE.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00041; fn3; 3.  
DR Pfam; PF00047; Ig\_3.  
DR PRINTS; PR00014; FNTYPEIII.  
DR SMART; SM00060; FN3; 3.  
DR SMART; SM00409; Ig\_2.  
DR SMART; SM00408; IGC2; 2.  
DR SMART; SM00406; IGv\_2.  
DR PROSITE; PS50835; IG-LIKE; 2.  
KW Hypothetical protein; Immunoglobulin domain; Repeat.  
SQ SEQUENCE 570 AA; 62110 MW; 45CEBDB5B340195 CRC64;  
Query Match 8.8%; Score 116.5; DB 4; Length 570;  
Best Local Similarity 22.8%; Pred. No. 0.13;  
Matches 58; Conservative 32; Mismatches 95; Indels 69; Gaps 13;



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QY 33 KSDTVELTCTASQKSIQFHMKNSNOIKILGNQGSFLTKGSKLNDRADSRSLMDQGNF 92
DB 48 QGRTVFPFCECTKGNPQPAVEMQKE-----GSQNLFPNQPOPN-----SRCSVSPTEG- 96
QY 93 PLIIKNIKIEDSDTYICEVEDQKEVQLVFG-LTANSND---THLLOGQSLTTLLESPPG 148
DB 97 -LITITNIGRSDAGYICQ-----LTVAGSLIAQAQLEVTVDLTDRPPTIILGGPAN 147
QY 149 SSPSV-----QC-----RSPRGKNIQGGKTLVSQLELQDSGT 181
DB 148 QTLAVGTALLKCKATGDPPLVISMKEGFTFPGRPRA-TIOEOGTLQIKNLRIISPCT 206
QY 182 WTCVTVLQNKQKVERK-IDIVPRA-----SALPAPPTGSALPD-----PQTASALPD 226
DB 207 YTCVATSSSETSKSAVLDTESGATISKYDLSDLGPPSKPQVTDVTNKSVTLSMQGP 266
QY 227 PPAASALPALAVI 240
DB 267 TP--GTLPAASAVII 278

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## RESULT 88

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QY 072681 PRELIMINARY; PRT; 660 AA.
AC 072681;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Hypothetical protein DKFZp79D0163 (Fragment).
GN DKFZp79D0163.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Mambour R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fodor G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX337757; CAD97826.1; -.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 660 AA; 70374 MM; A6DSBLCS0CB8815 CRC64;

```

Query Match 8.8%; Score 116.5; DB 4; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 0.16;  
 Matches 52; Conservative 29; Mismatches 76; Indels 75; Gaps 11;

```

QY 27 KVVLGKGGDVELTCTASQKSIQFHMKNSNOIKILGNQGSFLTKGSKLNDRADSRSL 86
DB 433 KVVASFGQRTMTCTRAEGPPPAIEWQDQ-----PVSSPHQL 473
QY 87 WDQGNPLIKNLIKIEDSDTYIC-----EVEDQKEVQLVFG-LTANSPTHLLOGQSLT 140
DB 474 QPDS--LIVISRVAVEDGGFTYTCVAFNGQDRDQR-WVQLRLGSLT-----ISGLPPT 523
QY 141 LTESPPGSSPSVOC-----RSPRGKNIQGGKTLVSQLELQDSGT 174
DB 524 VTV--PGGDTARLLCVVAGSSVNRWNRNGLPVQADGHRVHVSQPDG-----TLITLNL 574
QY 175 ELQDSGWTCTVLQNKQK-----PFKIDIVPRASALPAPPTGSALPDQPTAS 222
DB 575 RARDEGSITCSAYGSSQAVSRSTEVKV-VSPAPTAQPDPERDCVDPPELAN 625

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## RESULT 89

```

QY 0865F2 PRELIMINARY; PRT; 739 AA.
AC 0865F2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

```

```

DE Adhesion molecule VCAM-1.
GN VCAM-1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN 1;
RP SEQUENCE FROM N.A.
RA Schnurr K., Banning A., Kupper D., Muller-Schmehl K.,
RA Brigelius-Flohe R.;
RT Modulation of basal and interleukin-1-induced adhesion molecule
RT expression by phospholipid hydroperoxide glutathione peroxidase and
RT 15-lipoxygenase in rabbit aortic smooth muscle cells.
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AF212510; AAO52742.1; -.
DB GO; GO:0016020; C:membrane; IEA.
DB GO; GO:0016337; P:cell-cell adhesion; IEA.
DB InterPro; IPR003987; ICAM_VCAM-1.
DB InterPro; IPR003599; Ig.
DB InterPro; IPR007110; Ig-like.
DB InterPro; IPR003598; Ig_c2.
DB InterPro; IPR003989; VCAM-1.
DB Pfam; PF00047; Ig_5.
DB PRINTS; PR01472; ICAMVCAM1.
DB SMART; SM00409; IG_5.
DB SMART; SM00408; IG_c2_5.
DB PROSITE; PS50835; IG_LIKE; 5.
SQ SEQUENCE 739 AA; 81806 MM; 7AD0D32511E19342 CRC64;

```

Query Match 8.8%; Score 116.5; DB 6; Length 739;  
 Best Local Similarity 21.9%; Pred. No. 0.18;  
 Matches 50; Conservative 32; Mismatches 69; Indels 77; Gaps 9;

```

QY 32 KKGDTVELTCTASQKSIQFHMKNSNOIKILGNQGSFLTKGSKLNDRADSRSLMDQGN 91
DB 237 QEGSVTMTCSBGLVPEIFW-----SKQDNGLQRL---SGN 273
QY 92 PLIIKNIKIEDSDTYICEVEDQ-----KEVQLVFG-LTANSPTHLLOGQSLTTLLESPP 147
DB 274 ATLTLTAMWEDSGIVCEGVNOIGKSRKEVELIV-----QEKPTVEISP 319
QY 148 G-----SSPVQCSPPRGKNIQGGKTLVSQLELQDSG 180
DB 320 GPRIAQIDGPVLTCSVGCETPSRWRTQDPSLNGQVTSGLTSLTSSVSPRENEH 379
QY 181 TWTCTVLQNKQKVEFKIDI---VPR--ASALPAPPTGSALPDQPTAS 222
DB 380 SYLCTVTCGKHKLEKGIQVELYSFPRDPEILSGPVGNR---PVTVS 424

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## RESULT 90

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QY 095428 PRELIMINARY; PRT; 1235 AA.
AC 095428;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Abbasi N., Dors M., Ratcliffe A.,
RA Madan A., Dickhoff R., Shaffer T., James R., Laeky S., Hood L.;
RT "Complete sequence of the gene for presenilin 1."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF109907; AAC97963.1; -.
DR HSSP; P12111; 2KNT.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR007110; Ig-like.

```



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DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR002223; Kunitz_BPTI.
DR InterPro: IPR000884; TSP1.
DR Pfam: PF00047; Ig_3.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR Pfam: PF00090; Isp_1; 5.
DR PRINTS: PR00759; BASICPASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00408; IGc2; 3.
DR SMART: SM00131; KU; 1.
DR SMART: SM00209; TSP1; 5.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE: PS50835; IG_LIKE; 3.
DR PROSITE: PS50092; TSP1; 5.
DR Hypothetical protein; Immunoglobulin domain; Protease inhibitor;
KW Serine protease inhibitor.
SQ SEQUENCE 1235 AA; 133477 MW; A0B44CE4F3BE350 CRC64;

Query Match 8.8%; Score 116.5; DB 4; Length 1235;
Best Local Similarity 22.4%; Pred. No. 0.36; Mismatches 76; Indels 75; Gaps 11;
Matches 52; Conservative 29;

DR 27 KVLLEKKGDTVELTCTASQKSIQFHWKNSQIKILNQGSFLTKGPSKLNDRADSRSL 86
DB 1008 RLVDAAPGQRIRMTCRAGFPPEPALEWQRDQ-----PVSSPRRQL 1048
QY 87 WDQGNFLIIKNLKIEDSDTYIC-----EVEDQKEVOLLVFG-ITANSDFHLQGSGLT 140
DB 1049 QPDGS--LVISRAVEDGDFYTCVAFNGQDRDQR-WVQLRVLGELT-----ISGLPPT 1098
QY 141 LTLESPPGSSPSVOC-----RSPRKNIQSGKTLVSQSL 174
DB 1099 VTV--PESDTARLLCVVAGESVNIWNSNGLPVQADGRVHQSPPG-----TLITLNL 1149
QY 175 ELQDSGTCTVQLNQKQKTV---EFKIDIVPRASALPAPTCGSLPDPQTAS 222
DB 1150 RAPDGSYTCGAYQGSQAVNSRSTEVK-VSPAFTQAPRDPGRDCVQDELAN 1200

RESULT 91
Q9HCK4 PRELIMINARY; PRT; 1380 AA.
AC Q9HCK4.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein KIAA1568 (Fragment).
GN KIAA1568.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20450683; PubMed=1097877;
RA Nagase T., Kikuno R., Nakayama M., Hirosewa M., Onara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVIII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro.";
RL DNA Ref. 7:273-281(2000).
DR EMBL; AB046788; BABJ3394.1; -.
DR HSSP; P56276; IYTK.
DR Genew; HGNC:10250; ROBO2.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR007110; IG_LIKE.
DR InterPro: IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGc2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.

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KW Hypothetical protein; Immunoglobulin domain.
FT NON TER 1 151426 MW; 45E63B2EFA26732 CRC64;
SQ SEQUENCE 1380 AA; 151426 MW; 45E63B2EFA26732 CRC64;

Query Match 8.8%; Score 116.5; DB 4; Length 1380;
Best Local Similarity 22.8%; Pred. No. 0.42;
Matches 58; Conservative 32; Mismatches 95; Indels 69; Gaps 13;

QY 33 KGDVELTCTASQKSIQFHWKNSQIKILNQGSFLTKGPSKLNDRADSRSLMDQNF 92
DB 329 QGRTVTPPCETKGNPQPAVEWQKE-----GSQNLLEPNOQPN---SSCSVPTSD- 377
QY 93 PLIKNLKIEDSDTYICEVEDQKEVOLLVFG-ITANSDFHLQGSFLTKGPSK 148
DB 378 -LITNTIQRSDAGYITCA-----LTVAGSLIAKQLEVTVDLDRPPPIILQGAN 428
QY 149 SSPSV-----QC-----RSPRKNIQSGKTLVSQLEQDSGT 181
DB 429 QTLAVDGTALKCATGDPFLVISMKEGFTFPGRDPRA-TIQEGTLQINLRISPTGT 487
QY 182 WTCIVLQNKVERK--IDIVPRA-----SALPAPPGSLPDP---PQTASALPD 226
DB 488 YTCVATSSSGETSSAVLDVTEGATISKNYLSLDLPQPSKPPQVTVTKNSVTLSWQPG 547
QY 227 PPAASALPALAVI 240
DB 548 TP--GTLPAAYII 559

RESULT 92
Q8NAO3 PRELIMINARY; PRT; 354 AA.
AC Q8NAO3.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ34988.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Nihi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Salto K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Magatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK092307; BAC03858.1; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG_LIKE.
DR InterPro: IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGc2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 354 AA; 38779 MW; 5DC938094E35964A CRC64;

Query Match 8.8%; Score 116; DB 4; Length 354;
Best Local Similarity 22.6%; Pred. No. 0.078;
Matches 52; Conservative 36; Mismatches 94; Indels 48; Gaps 10;

QY 20 PAATQGNKVLVIGKGDVELTCTASQKSIQFHWKNSQIKILNQGSFLTKGP-----SK 75
DB 41 PMAAVDMMV--RKGDPAVLRCTYLEDGA--KGALNRSIIIFAG--GDKNSVDPRAVIST 95
QY 76 LNDRADSRSLMDQGNFLIIKNLKIEDSDTYICEVEDQKEVOLLVFGTLA----- 127

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Db      96 LNKR-----DYSLOQNVDDDPYTCVOTQTPRTMOYH-LTVQVPPKIYD 143
Qy      128 -NSDTHLLQSGSLTLTLESPPGSSPVQCR--SPRGKNIQGGKTLVSQLELQDSTWTC 184
      144 ISNDMTVEGNTVTLTCLATGKPEPFISWHISPSAPFNQGLDIYGTTRQAGYEYC 203
Qy      185 TV-----LQNKVKEFKIDIVPRASALPAPT-----GSLALPD 218
      204 SAENDVSFPDVRRKVVNPAFTIQEIKSGTVTPGRSGLIRCEGAVPPP 253
Db

RESULT 93
Q991A6 PRELIMINARY; PRT; 484 AA.
ID Q991A6
AC Q991A6
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003495; AA03495.1; -.
DR PIR; F33932; F33932.
DR HSSP; P01810; 2RBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 484 AA; 52567 MW; 8BEA4F9BCF582PA CRC64;

Query Match      8.8%; Score 115.5; DB 11; Length 484;
Best Local Similarity 23.3%; Pred. No. 0.13;
Matches 70; Conservative 32; Mismatches 117; Indels 81; Gaps 12;

Qy      13 VLQALLPAATQGNKV-----VLGKGDVLTCTASQKKSIGF--HMKNNOIKI 61
      4 VMTLLFLFMAAQAQSIQAIQLVQSGPELKKGEIVKISCKASGYFTDYSMMWVQAQPKG 63
Db
Qy      62 LGNGSF-LTKGPEKLNDRADSRSL---MDQGFPLIKLKIEDSDTYICEVEDQKE 117
      64 LKMWGWNIEGESVYADDFKGRPAFSLSTASTIHLQINNLKNEIDATATYFCARSDYD 123
Db
Qy      118 VOLLVFGLTANSDFHLQSGSLTLTLES-----PPGSS-----PS 152
      124 IYAM-----DYMGQGSIVTVSSSASNPITYPLTLPALSSDVIIICGLIHDPFS 174
Db
Qy      153 VQCSPPGKN-----IQGKTLVSQLELQDSTWTCVTVLQNKVE 194
      175 GTMNVTVGKSGKQDITTVNFPALASGGRYTWSQLTTPAVECPGESVSKSVQGHDSIPVQ 234
Db
Qy      195 FKIDIVPRASALPAPPGSALPDPQTSALPDPRAALAVIFLGLGLGAVACVL 254
      235 -ELDV---NCSGTPPPPTITPSCQPSLISQRP-----ALEDLLGSDASTICTL 280
Db

RESULT 94
Q97PD3 PRELIMINARY; PRT; 820 AA.
ID Q97PD3
AC Q97PD3
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

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DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo W.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Miliady S.J.,
RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleja U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Brain;
RA Strauberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055333; AAH55333.1; -.
KM Hypothetical protein.
SQ SEQUENCE 820 AA; 90951 MW; ECB1F6D26983065E CRC64;

Query Match      8.8%; Score 115.5; DB 11; Length 820;
Best Local Similarity 23.6%; Pred. No. 0.26;
Matches 60; Conservative 28; Mismatches 97; Indels 69; Gaps 13;

Qy      33 KQDVELTCTASQKKSIGFHMKNNOIKILGNGSFLTGPSKLNDRADSRRLMDQGNF 92
      331 QGRTVPPEETKKNPPAVFWQK-----GSGNLLFPNQDQPN---SRCSVSPGTD- 379
Db
Qy      93 PLIKNKLIKIEDSDTYICEVEDQKEEVLVFG-----LTANSDFHLQSG-- 136
      380 -LITNIGRSDAQYVICAQ-----LVAGSIILAKQLEVTVDLTDRPPIILQGPIN 430
Db
Qy      137 QSL-----TITLESPPGSSP-----SVQCRSPRGKNIQGGKTLVSQLELQDSTG 181
      431 QTLAVDGTALLKCKATGEBLPVLSWLKEGFTFLGRPRA-TIQQDQTLQIKNLRIIDTGT 489
Db
Qy      182 WTCVTVLQNKVKEFK--IDIVPRASA-----LPAPPGSALPDPQ---TASALPD 226
      490 YTCVATSSSGEFTSWSAVLDVTESGATISKYVDMNDLPGPSKQVTVDSKNSVTLWSQPG 549
Db
Qy      227 PPAASALPALAVI 240
      550 TP--GVLPAASAVII 561
Db

RESULT 95
Q9VY33 PRELIMINARY; PRT; 344 AA.
ID Q9VY33
AC Q9VY33; Q9VSR2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE CG32600 protein (GH05565p).
GN CG32600 OR CG5291 OR CG14477 OR CG144415.
OS Drosophila melanogaster (Fruit fly).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OK NCBI\_taxid=7227?  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley.  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanaides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandeell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson S.K., Miklos G.L.G.,  
RA Abell J.F., Agbayani A., An H.-C., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Baau A.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
RA Borokov D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burris K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Dey A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harvie N.L., Harvey D., Heiman T.J., Hernandez J.H., Honck J.,  
RA Hootin D., Houston K.A., Howland T.J., Mei M.-H., Ibeagwa C.,  
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Liao P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattet B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacel J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,  
RA Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stepieton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasarman D.A., Weisbach G.M., Weissbach J.,  
RA Williams S.M., Wozniak T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith R.O.,  
RA Gibbs X.H., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:12185-12195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Amanaides P.G., Brandon R.C., Rogers Y.,  
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Buesam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorest V., Doup L.E., Doyle C., Drenek D., Farfan D.,  
RA Ferreira S., Frisbe E., Galle R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Honck J., Hoskins R.A., Hootin D., Howland T.J.,  
RA Ibeagwa C., Jaitai M., Kruse D., Li P., Mattet B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
RA Pacel J., Paragas V., Park S., Patel S., Pfeiffer B.,  
RA Phouanavong S., Pittman G.S., Puti V., Richards S., Scheeler F.,  
RA Stepieton M., Strong R., Svirskas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RL "Sequencing of *Drosophila melanogaster* genome."  
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RP [3]  
RP SEQUENCE FROM N.A.  
RA Mira S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
RA Tudy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,  
RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
RT "Annotation of *Drosophila melanogaster* genome."

RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RA	Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;	
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	
RN	[5]	
RP	SEQUENCE FROM N.A.	
RA	FlyBase;	
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.	
RN	[6]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-Berkeley.	
RA	Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,	
RA	Champe M., Chavez C., Dorsett V., Fafian D., Flise E., George R.,	
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,	
RA	Nunoo J., Pacleob J., Paragas V., Park S., Phouenavong S., Wan K.,	
RA	Yu C., Lewis S.E., Rubin G.M., Celniker S.,	
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AE003495; AAF48372.2; -	
DR	EMBL; AY060637; ALA28185.1; -	
DR	FlyBase; FBgn0052600; CG32600.	
DR	InterPro; IPR003599; IG	
DR	InterPro; IPR007110; IG_1like.	
DR	InterPro; IPR003598; IG_c2.	
DR	Pfam; PF00047; IG_2.	
DR	SMART; SM00409; IG_2.	
DR	SMART; SM00408; IGC2; 2.	
DR	PROSITE; PS50835; IG_LIKE; 2.	
KW	Immunoglobulin domain.	
SO	SEQUENCE 344 AA; 37611 MW; BF259D7CB612F24C CRC64;	

Query Match	Similarity	8.7%	Score 115;	DB 5;	Length 344;
Best Local	Similarity	23.5%	Pred. No.0.092;		
Matches	60;	Conservative	31;	Mismatches 113;	Indels 52; Gaps 12
Qy	29	VLGKKGDVLELTCTASQKKS	IQFHKXNSNQIKLGNQSG	FLTKGPKSLNDRASRRSIWD	88
Db	52	ITGVGKTVKLTCTRVKLN	GNRTVSAVWRHDIHL	TVGRYYTSPDQREAHMS	PAABDW 109
Qy	89	QGNFPLIIKMLKIDSDTY	ICEVEDQ-----	EEVQLVFGLTASDTHLLGQ	137
Db	110	---TLRIYARQKDSGI	ECQISTTPPIGHSVY	LNIVEPVTDIIG---	PELHINRGS 161
Qy	138	SLITTL-----	ESPP-----	GSSPSVQCRSPRG-----	KNIQGKTLISVQLELQDS 179
Db	162	TINTLCYKFAPEPPPTV	IWSHNEIINIFSDPRG	ISLVTEKGVLTSRLLVQKAI	TQDS 221
Qy	180	GTWCTCYLQNKQKVEFK	DIY--PRASALPAPPPG	SALPDQOTASALPDPPASAL	PAAL 237
Db	222	GLYICTP--SNNP	TSVRAHIVDGEHP	AMHTGNNGNS-----	TAS---QPPV--LLPIVL 270
Qy	238	AVISFLGLGLGVAC	252		
Db	271	LTCSTIMLQLVASC	285		
RESULT 96					
Q723Y4					
ID	Q723Y4	PRELIMINARY;	PRT;	236	AA.
AC	Q723Y4;				
DT	01-OCT-2003	(TREMBLrel. 25, Created)			
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
BN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skeletal muscle;				
FX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				

RA Kjauner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,  
 RA Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bogak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,  
 RA Krzywnski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC005332; AAI05332.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;  
 Query Match 8.7%; Score 114.5; DB 4; Length 236;  
 Best Local Similarity 28.6%; Pred. No. 0.062;  
 Matches 57; Conservative 20; Mismatches 77; Indels 45; Gaps 10;  
 QY 11 LVLVQLALPAA-----TGANKVYLGGKGPVLTCTASQKSIQFMWNSNQIKLGN 64  
 DB 9 ILGLILLCPGARDICMTQSPSSLSASVSDVTVTITRASQDISNYLAWFQOKP---GK 64  
 QY 65 QGSFLTGPKSLNDRADSRSLMDQG-NFPLIINKLIEISDPYICEVEDQKEEVQLLV 123  
 DB 65 APTSILYIGASSLSGSGVSKSGSGGTFITLITSSLDPEPFIATYCC---QQTKSYVTF 120  
 QY 124 GLTANSDTHLLQGSLTLTLTLESPGSSPVQCSPPKSKNIQGGKTLVSQLELDGSGTW 183  
 DB 121 G-----GGTKLEI---KRTVAAPSVFIFPPSDEQLKSG-TASV-----V 155  
 QY 184 CTVLQN---QKKVEFKID 198  
 DB 156 C-LINNFYPREAKVQMKVD 173  
 RESULT 97  
 Q8UUG3 PRELIMINARY; PRT; 308 AA.  
 AC Q8UUG3;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Novel immune-type receptor 2.  
 GN NITR2.  
 OS Ictalurus punctatus (Channel catfish).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Siluriformes;  
 OC Ictaluridae; Ictalurus.  
 NC NCBI\_TaxID=7998;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21574523; PubMed=11698645;  
 RA Hawke N.A., Yoder J.A., Haire R.N., Mueller M.G., Litman R.T.,  
 RA Miracle A.L., Stuge T., Shen L., Miller N., Litman G.W.;  
 RT "Extraordinary variation in a diversified family of immune-type  
 RT receptor genes";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:13832-13837(2001).  
 DR EMBL: AF397467; AAL35555.1; -  
 DR EMBL: AF397455; AAL35543.1; -

DR GO:0004872; F:receptor activity; IEA.  
 DR InterPro: IPR003559; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR Pfam: PF00047; Ig1.2.  
 DR SMART: SM00409; Ig1.2.  
 DR PROSITE: PS50835; IG\_LIKE; 2.  
 KW Receptor.  
 SQ SEQUENCE 308 AA; 34259 MW; A1AD3192157A572 CRC64;  
 Query Match 8.7%; Score 114.5; DB 13; Length 308;  
 Best Local Similarity 21.7%; Pred. No. 0.088;  
 Matches 55; Conservative 35; Mismatches 88; Indels 75; Gaps 11;  
 QY 10 LVLVQLALPAA-----GSKNVYLGGKGPVLTCTASQKSIQFMWNSNQIKLGN 63  
 DB 7 ILLCEPLHLVKTQTPRNSDSLVPFAEGDSVNSICTYESDMMHMFQYKYNIGQKPKLIS 66  
 QY 64 NQGSFLTGPKSLNDRADSRSLMDQG-NFPLIINKLIEISDPYICEVEDQKEEVQLLV 122  
 DB 67 NPKYDKKATPHEPERNNARFPMVNEKSKTNLEIKGLQSDATYFC---GSANSHIVE 122  
 QY 123 FG---LTANSDTHLLQGSLTLTLTLESP-----PGSSPSVOC-----R 156  
 DB 123 FGSGTELVVQASQSHLS-----VLQQPVHELHPGGSYTLHCTVITDRCAGHSVYMPR 176  
 QY 157 SERG-----KNIQGGK-----TLSVQLDLDGSGTWCTV----- 186  
 DB 177 HNSGSEHPGVITYHDSNGRCCKNPAGSLTMCVYSLPKTNLSTSDVGTYHCAVAACQ 236  
 QY 187 --LQNKVEFKI 197  
 DB 237 ILFGNCKLDMKI 249  
 RESULT 98  
 Q96SC3 PRELIMINARY; PRT; 2673 AA.  
 AC Q96SC3;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Fibulin-6 (Fragment).  
 GN FIBL-6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Melanoma;  
 RA Kostka G., Timpi R.;  
 RT "Partial sequence of fibulin-6 with a C-terminal region related to  
 RT domain II and III of the fibulin family";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ306906; CAC37630.1; -  
 DR GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro: IPR00152; Asx\_hydroxyl\_S.  
 DR InterPro: IPR00875; Cecropin.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR006209; EGF\_Like.  
 DR InterPro: IPR009017; GFP\_Like.  
 DR InterPro: IPR007110; Ig-Like.  
 DR InterPro: IPR003558; Ig\_C2.  
 DR InterPro: IPR00884; TSP1.  
 DR InterPro: IPR008085; TSP1.  
 DR Pfam: PF00048; EGF\_5.  
 DR Pfam: PF00047; Ig1.7.  
 DR Pfam: PF00090; TSP1.6.  
 DR PRINTS: PR01705; TSP1REPEAT.  
 DR SMART: SM00479; EGF\_CA; 7.  
 DR SMART: SM00408; IGC2; 7.  
 DR SMART: SM00209; TSP1; 6.  
 DR PROSITE: PS0010; ASX\_HYDROXYL; 5.

DR PROSITE; PS00268; CECROPIN; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 8.  
 DR PROSITE; PS50835; IG\_LIKE; 17.  
 DR PROSITE; PS50092; TSP1; 6.  
 KM EGF-like domain; Immunoglobulin domain.  
 FT NON TER  
 SQ SEQUENCE 2673 AA; 291017 MW; BEAEC30B8340E272 CRC64;

Query Match 8.7%; Score 114.5; DB 4; Length 2673;  
 Best Local Similarity 20.9%; Pred. No. 1.5;  
 Matches 66; Conservative 40; Mismatches 93; Indels 117; Gaps 13;

QY 1 MNRGVPRHLLVQLLPPAATGQNKVVLGKGGDTVELTCTASQKSIOPHMKN----- 55  
 DB 415 LKNDLP---LPLSHIRLL-NAGGVIRIVRAQVSDVAVYTVASNRAGVNDKHYNLQVFA 470  
 QY 56 -SNOIKILGNQSEFLTKGPKS---LNDRADSRSLMDQGNFPL-----11K 97  
 DB 471 PRMNDNMGTREIIVLKGSSVSMACITDGTAPSMAMLRDQQLGLAHILVSTHGMVLQ 530  
 QY 98 NLK--IEDSTYIC-----EV-----EDQKEEVOLLV----- 122  
 DB 531 LLKAEEDSGKYTCIASNEAGEVSKHFLKYLEPPHNGSEHEIEIVVNNPLELTICIA 590  
 QY 123 FGLTANSDTHLQOQSLLTLIESPSSPSVQCSPRGKNIQGGKTLVSQLELDSDGTW 182  
 DB 591 SGIPAPKMTWKDRIPLPQT-----DOVQTGGGEVARISTAQVEDTGRY 635  
 QY 183 TC-----TVLQN-QKTYEFKIDIVPRASALPAP 209  
 DB 636 TCLASSPAGDDKREYLVKRVHPNVIAGTDEPRDITVLNRQVTLKESDAVP-----P 688  
 QY 210 PTGSALPDPOQTASALP 225  
 DB 689 PVITWLNNGERLQATP 704

## RESULT 99

QY 0723W6 PRELIMINARY; PRT; 338 AA.  
 AC 0723W6;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein DKFZP686H1949.  
 GN DKFZP686H1949.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Human amygdala;  
 RA Wamburt R., Heubner D., Mewes H.W., Well B., Amid C., Oeanger A.,  
 RA Fobio G., Han M., Wiemann S.,  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BX517377; CAD97619.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 338 AA; 37267 MW; EDD86BE2C57B09E3 CRC64;

Query Match 8.7%; Score 114; DB 4; Length 338;

Best Local Similarity 23.0%; Pred. No. 0.11;

Matches 59; Conservative 41; Mismatches 101; Indels 56; Gaps 11;

QY 4 GVPFRHLLVQLLPPAATGQNKVVLGKGGDTVELTCTASQKSIOPHMKNSNOIKILG 63  
 DB 21 GVPFRS-----GDATFPKAMN---VTVQGESATLKTIDRYT-RVAMLNRSITILYAG 71  
 QY 64 N-----QGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEV--- 112  
 DB 72 NDKWSIDBRVILVNTFTQ-----YSIMIGNVDVYDEGPTCSVQTDNH 115

QY 113 DQKEVOLLVFG---LTANSDTHLQOQSLLTLIESPSSPSVQCSPRGKNIQ--- 165  
 DB 116 PKTSRHLLIVQVPRQIMNISDITVNEGSSVTLICLAGRPETVTRHLSVNEGQFVS 175  
 QY 166 -GKTLVSQLELDSDGTWTCTVLO---NOKYEFKIDIVPRASALPAPPTGSALPDPO 219  
 DB 176 EDEVLFIISDIDKROQSGEYCSALNDVAAPVRKVKITVNPYPYIS--KAKNTGVSVQOK 233  
 QY 220 TASALPDPPASALPAP 236  
 DB 234 ILSC-----BASAVPMA 245

## RESULT 100

QY 08N3J6 PRELIMINARY; PRT; 435 AA.  
 AC 08N3J6;  
 DT 01-OCT-2002 (TREMBLrel. 22, Created)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN DKFZP761G128.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Amalgala;  
 RA Koehler K., Beyer A., Mewes H.W., Well B., Wiemann S.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; ALG34270; CAD38945.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; IG\_3.  
 DR SMART; SM00409; IG\_2.  
 DR SMART; SM00408; IGC2; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR KW Hypothetical protein; Immunoglobulin domain.  
 SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D446 CRC64;

Query Match 8.7%; Score 114; DB 4; Length 435;

Best Local Similarity 21.6%; Pred. No. 0.15; Indels 82; Gaps 13;

Matches 58; Conservative 40; Mismatches 88; Indels 82; Gaps 13;

QY 33 KGDVELTCTASQKSIOPHMKNSNOIKIL-----GNQGSFLTKGPKSLNDRADSR 83  
 DB 138 EGDLMQTLCTGSGSKPAADIRMFNDKEIKDVKYLKEDANRKTFTVS--STLDFRVD-- 193  
 QY 84 RSLMDQGNFPLIKNLKIEDSDTYICEVEDOK---EVQLLPFGLTANSDTHL----- 134  
 DB 194 -----RSDGVAVICRVHDSINATPQVAMQVLEIHYTPSVKLIPTPF 237  
 QY 135 --QGSLLTLIESPSSPSVQCSPRG-----KNIQGGKTLVSQLELDSDGTCTC- 184  
 DB 238 PQESQPLILTCESGKFLPEVATMTKDGGLPDPDRVWVSGRELNIPLFKNTDNGITRCE 297  
 QY 185 -TVLQNKYEFKIDIVPRASALPAPPTGSALPDPOQTASA 223  
 DB 298 ATNTIGSSASAEVLIIVDVENTLLPTIISLTATVTTVALITTSPTTSA-----TTSS 352  
 QY 224 LPDP-----PASALPALAVISFL 243  
 DB 353 IRDPNALAGONGPDHALIGIVAVVAV 380

Search completed: August 3, 2004, 13:13:40  
 Job time : 22.7158 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2004, 12:50:09 ; Search time 26.2483 Seconds  
(without alignments)  
2777.216 Million cell updates/sec

Title: SE06  
Perfect score: 1317  
Sequence: 1 MNRGVPRHLLVLQLALP.....VISFLGLGVACVLAARR 258

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 125 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1041.5	79.1	449	6	AAE37576 Human FDI
2	1038	78.8	310	2	AAE37576 Human FDI
3	1038	78.8	310	2	AAE37576 Human FDI
4	1038	78.8	310	2	AAE37576 Human FDI
5	1038	78.8	310	2	AAE37576 Human FDI
6	1038	78.8	310	2	AAE37576 Human FDI
7	1038	78.8	310	2	AAE37576 Human FDI
8	1038	78.8	310	2	AAE37576 Human FDI
9	1038	78.8	310	2	AAE37576 Human FDI
10	1038	78.8	310	2	AAE37576 Human FDI
11	1038	78.8	310	2	AAE37576 Human FDI
12	1038	78.8	310	2	AAE37576 Human FDI
13	1038	78.8	310	2	AAE37576 Human FDI
14	1038	78.8	310	2	AAE37576 Human FDI
15	1038	78.8	310	2	AAE37576 Human FDI
16	1038	78.8	310	2	AAE37576 Human FDI
17	1038	78.8	310	2	AAE37576 Human FDI
18	1038	78.8	310	2	AAE37576 Human FDI
19	1038	78.8	310	2	AAE37576 Human FDI
20	1038	78.8	310	2	AAE37576 Human FDI
21	1038	78.8	310	2	AAE37576 Human FDI
22	1038	78.8	310	2	AAE37576 Human FDI
23	1038	78.8	310	2	AAE37576 Human FDI
24	1038	78.8	310	2	AAE37576 Human FDI
25	1038	78.8	310	2	AAE37576 Human FDI

26	1029	78.1	402	1	AAE37576 Human FDI
27	1029	78.1	402	1	AAE37576 Human FDI
28	1029	78.1	402	1	AAE37576 Human FDI
29	1029	78.1	402	1	AAE37576 Human FDI
30	1029	78.1	402	1	AAE37576 Human FDI
31	1029	78.1	402	1	AAE37576 Human FDI
32	1029	78.1	402	1	AAE37576 Human FDI
33	1029	78.1	402	1	AAE37576 Human FDI
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45	1029	78.1	402	1	AAE37576 Human FDI
46	1029	78.1	402	1	AAE37576 Human FDI
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83	1029	78.1	402	1	AAE37576 Human FDI
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85	1029	78.1	402	1	AAE37576 Human FDI
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87	1029	78.1	402	1	AAE37576 Human FDI
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94	1029	78.1	402	1	AAE37576 Human FDI
95	1029	78.1	402	1	AAE37576 Human FDI
96	1029	78.1	402	1	AAE37576 Human FDI
97	1029	78.1	402	1	AAE37576 Human FDI
98	1029	78.1	402	1	AAE37576 Human FDI

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99 946 71.8 458 2 AAR15149 Aar15149 CD4 coord
100 916 69.6 394 1 AAP90833 Aap90833 Amino aci
101 916 69.6 434 1 AAP96151 Aap96151 Sequence
102 916 69.6 434 1 AAP93557 Aap93557 Fusion of
103 916 69.6 729 2 AAR41042 Aar41042 CD4-GRPH
104 916 69.6 942 2 AAR41041 Aar41041 CD4-GSP13
105 916 69.6 1786 2 AAR41043 Aar41043 CD4-SBA17
106 914 69.4 410 2 AAW35860 Aaw35860 Human CD4
107 912 69.2 458 2 AAR20148 Aar20148 Cynomolgus
108 910 69.1 400 2 AAR20149 Aar20149 Sol. rhcs
109 909 69.0 458 2 AAR10987 Aar10987 Rhesus mo
110 905 68.7 375 2 AAR07721 Aar07721 Recombina
111 903 68.6 333 2 AAR04926 Aar04926 Immunopro
112 903 68.6 435 2 AAP90992 Aap90992 Human CD4
113 901.5 68.5 549 2 AAR04920 Aar04920 Immunopro
114 901.5 68.5 557 2 AAR04923 Aar04923 Immunopro
115 899 68.3 178 6 ABU07701 Abu07701 Viral coa
116 899 68.3 185 2 AAY14206 Aay14206 HIV-1 gp1
117 899 68.3 195 2 AAY14210 Aay14210 HIV gp120
118 899 68.3 217 2 AAR15150 Aar15150 PCDA-gels
119 899 68.3 369 2 AAY39824 Aay39824 Soluble h
120 899 68.3 369 3 AAY68327 Aay68327 T4 glycop
121 899 68.3 370 1 AAP93528 Aap93528 Human sol
122 899 68.3 370 4 AAB83356 Aab83356 Human CD4
123 899 68.3 433 3 AAY54500 Aay54500 Amino aci
124 899 68.3 530 6 ABU07697 Abu07697 Viral coa
125 899 68.3 720 6 ABU07694 Abu07694 Viral coa

```

## ALIGNMENTS

## RESULT 1

AAE37576 standard; protein: 449 AA.

AAE37576;

27-AUG-2003 (first entry)

Human FDI2-Ig alphatp fusion protein variant.

Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig;  
 human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; DI;  
 D2; alpha tailpiece; alphatp; fusion protein; muten; variant; mutant.

Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 218 /note= "Wild type Glu substituted with Pro"

FT Misc-difference 219 /note= "Wild type Leu substituted with Val"

FT Misc-difference 221 /note= "Wild type Gly substituted with Ala"

MO2003040311-A2.

15-MAY-2003.

24-OCT-2002; 2002WO-US034393.

25-OCT-2001; 2001US-0346231P.

(USSH ) US DEPT HEALTH &amp; HUMAN SERVICES.

Archos J, Cicala C, Fauci AS;

WPI; 2003-441545/41.

N-PSDB; ACG82877.

New CD4 polypeptide ligated at its C-terminus with a portion of an  
 immunoglobulin, useful for preparing a composition for treating or

PT preventing HIV-1 infection.

XX Example 11; Page 67; 100pp; English.

XX The invention relates to a CD4 (cluster of differentiation factor 4)  
 polypeptide ligated at its C-terminus with a portion of an immunoglobulin  
 (Ig) comprising a hinge region and a constant domain of a mammalian Ig  
 heavy chain. The polypeptide comprises a tailpiece from the C-terminus of  
 the heavy chain of an IgA or IgM antibody. Polypeptides of the invention  
 are useful for preparing a composition for treating or preventing human  
 immunodeficiency virus (HIV)-1 infection. The invention is useful in gene  
 therapy and also in the preparation of vaccines. The present sequence is  
 a fusion protein variant (G218P/L219V/220delA/G221A) which comprises a  
 human IgA alpha tailpiece (alphatp), a human IgG2 constant region  
 comprising a hinge, a CH2 and CH3 region and a human CD4 D1D2 domain.  
 CC This variant protein is also referred to as mutant F

SQ Sequence 449 AA;

Query Match 79.1%; Score 1041.5; DB 6; Length 449;

Best Local Similarity 85.4%; Pred. No. 2.4e-64; Matches 210; Conservative 6; Mismatches 17; Indels 13; Gaps 3;

QY 1 NMRGVPFRLHLVLTALIPAAATQGNKYLGKKGVETELCTASOKKSIQFMKNSNQIK 60

DB 1 NMRGVPFRLHLVLTALIPAAATQGNKYLGKKGVETELCTASOKKSIQFMKNSNQIK 60

QY 61 ILNGSGFLTKGSPSLNDRADSRSLMDQGNPPLIKKLTEDSPYICEVDQKEEYOL 120

DB 61 ILNGSGFLTKGSPSLNDRADSRSLMDQGNPPLIKKLTEDSPYICEVDQKEEYOL 120

QY 121 LVFGLTANSDFHLQGGSLTLTLESPPSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

DB 121 LVFGLTANSDFHLQGGSLTLTLESPPSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

QY 181 TWCTVLTQNKQKVERKIDIVPPASA-----LPAPP-TGSAL----PDPTGASALPFP 227

DB 181 TWCTVLTQNKQKVERKIDIVLASADKTHTCPPCAPVAPSVFLFPKPKDITLMSRT 240

QY 228 PAASAL 233

DB 241 PEVTCV 246

## RESULT 2

AAR26784 standard; protein: 310 AA.

AAR26784;

24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 06-FEB-1993 (first entry)

CD4-IgG2 chimeric light chain.

homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;

chimeric; increased serum half life; HIV infection; AIDS; ss.

Homo sapiens.

Chimeric.

Key Location/Qualifiers

FT Domain 1..205 /label= CD4 domain

FT Domain 206..310 /label= Ckappa domain

MO9213947-A1.  
 20-AUG-1992.  
 10-FEB-1992; 92WO-US001143.



XX 08-FEB-1991; 91US-00653684.  
PR (PROG-) PROGENICS PHARM INC.  
XX Beaudry GA, Maddon PJ;  
XX WPI; 1992-300034/36.  
DR N-PSDB; AAQ28090.  
PT CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for  
XX treatment, prevention and diagnosis of HIV infection.  
XX  
PS Claim 16; Fig 5; 90pp; English.  
XX  
XX This sequence represents a CD4-IgG2 chimeric heavy chain heterotetramer  
CC it was produced by expression of the coding mutagenised cDNA (produced as  
CC described in AAQ28089) in Dhfr-CHO cells. The protein is efficiently  
CC assembled intracellularly and effectively secreted from mammalian cells  
CC pref. CHO, COS, or myeloma cells as a heterotetramer, enabling high  
CC recovery and purification from the medium of cells expressing it. It  
CC possesses increased serum half-life and has increased avidity for HIV cF.  
CC heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block  
CC the spread of HIV infection within a patient. Attachment to a detectable  
CC marker makes it useful in an assay for HIV or SIV infection, and it can  
CC also be linked to toxins, eg diphtheria, pseudomonas exotoxin A (domains  
CC I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003  
CC to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 310 AA;  
XX  
Query Match 78.8%; Score 1038; DB 2; Length 310;  
Best Local Similarity 85.7%; Pred. No. 2.8e-64;  
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;  
XX  
QY 1 MNRGVFRRHLVLVQLALIPATQGNKVLGKKGDTVELTCTASQKKSIOFHKNSNOIK 60  
Db 1 MNRGVFRRHLVLVQLALIPATQGNKVLGKKGDTVELTCTASQKKSIOFHKNSNOIK 60  
XX  
QY 61 ILGNQGSFLTKGSPSKUNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
Db 61 ILGNQGSFLTKGSPSKUNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
XX  
QY 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
Db 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
XX  
QY 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPPPPASALPALAVI 240  
Db 181 TWTCTVLQNKQKVEFKIDIVLAFTVAAP-----SVFIRPPSDQLKSGTASV 228  
QY 241 SFLL 244  
Db 229 VCLL 232  
XX  
RESULT 3  
AA46680 standard; protein; 310 AA.  
XX  
XX AA46680;  
XX  
XX 25-MAR-2003 (revised)  
DT 08-AUG-1994 (first entry)  
XX  
XX CD4-kappa light chain.  
XX  
XX CD4; gamma; heavy chain; chimeric; chimaeric; immunconjugate; HIV;  
KW human immunodeficiency virus; radionuclide; toxin; therapy; treatment;  
XX imaging; detection; targeting; immunoglobulin; IgG.  
XX  
XX Homo sapiens.  
XX

FH Key Location/Qualifiers  
FT Region 1..204  
FT /label= CD4 Region.  
FT Region 205..310  
FT /label= Kappa Region.  
XX  
XX MO9403191-A1.  
XX  
XX 17-FEB-1994.  
XX  
XX 06-AUG-1993; 93WO-US007422.  
XX  
XX 07-AUG-1992; 92US-00927931.  
XX  
XX (PROG-) PROGENICS PHARM INC.  
XX  
XX Allaway GP, Maddon PJ;  
XX  
XX WPI; 1994-065392/08.  
DR N-PSDB; AAQ57752.  
XX  
XX Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2  
PT immunoconjugates - used to kill HIV-infected cells and to image and  
XX stage HIV infection.  
XX  
PS Disclosure; Fig 5; 142pp; English.  
XX  
XX A tetramer comprising 2 IgG2 heavy chains or two CD4-IgG2 chimeric heavy  
CC chains (AA46679) and two kappa light chains or CD4-kappa light chains is  
CC linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide  
CC of low to moderate cytotoxicity. The resulting immunconjugate comprising  
CC the toxin can be used to kill HIV infected cells and to treat HIV  
CC infected subjects to reduce the population of HIV infected cells. It can  
CC also be used to reduce the likelihood of infection. The immunconjugate  
CC comprising the radionuclide can be used to image HIV infected tissue, to  
CC calculate the stage of HIV infection or the efficacy of an anti-HIV  
CC treatment using the imaging technique and for determining the prognosis  
CC of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 310 AA;  
XX  
Query Match 78.8%; Score 1038; DB 2; Length 310;  
Best Local Similarity 85.7%; Pred. No. 2.8e-64;  
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;  
XX  
QY 1 MNRGVFRRHLVLVQLALIPATQGNKVLGKKGDTVELTCTASQKKSIOFHKNSNOIK 60  
Db 1 MNRGVFRRHLVLVQLALIPATQGNKVLGKKGDTVELTCTASQKKSIOFHKNSNOIK 60  
XX  
QY 61 ILGNQGSFLTKGSPSKUNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
Db 61 ILGNQGSFLTKGSPSKUNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
XX  
QY 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
Db 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
XX  
QY 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPPPPASALPALAVI 240  
Db 181 TWTCTVLQNKQKVEFKIDIVLAFTVAAP-----SVFIRPPSDQLKSGTASV 228  
QY 241 SFLL 244  
Db 229 VCLL 232  
XX  
RESULT 4  
AA465081 standard; protein; 310 AA.  
XX  
XX AA465081;  
XX  
XX 19-JUN-2000 (first entry)  
XX

```

XX CD4-kappa chimeric light chain amino acid sequence.
DE
XX
KM CD4-kappa chimeric light chain; immunoglobulin; treatment: CD4-IgG2;
KW cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
KM cellular immune response interaction mediator; HIV interaction; staging;
KM prognosis; envelope glycoprotein burden; human.
XX
OS Homo sapiens.
PN US6034223-A.
XX
PD 07-MAR-2000.
XX
PF 07-JUN-1995; 95US-00477460.
XX
PR 07-AUG-1992; 92US-00927931.
PR 06-AUG-1993; 93WO-US007422.
PR 03-FEB-1995; 95US-00379516.
XX
PA (PROG-) PROGENICS PHARM INC.
PI Allway GP, Maddon PJ;
XX
DR MPI; 2000-269502/23.
DR N-PSDB; AA298857.
XX
PT New immunoglobulin, used to treat, prevent or image human immune
PT deficiency virus infection, comprises radionuclide attached to
PT heterotetramer of CD4-immunoglobulin chimera.
XX
PS Disclosure; Fig 5; 58pp; English.
XX
CC This sequence represents the CD4-kappa chimeric light chain amino acid
CC sequence of the CD4-IgG2 chimeric heterotetramer. The invention relates
CC to an immunoglobulin comprising a cytotoxic radionuclide and a
CC heterotetramer of two heavy chains and two light chains. The cytotoxic
CC radionuclide is linked to either the heavy chains or the light chains, or
CC to all four chains, directly or through a bifunctional chelator. Both
CC heavy chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by
CC vector CD4-IgG2HC-PRCMV (ATCC 75193) and both light chains are chimeric
CC CD4-kappa chains encoded by vector CD4-KLC-PRCMV (ATCC 75194). CD4 is a
CC non-polymorphic cell surface glycoprotein that is expressed on the
CC surface of helper T lymphocytes, cells of the monocyte/macrophage lineage
CC and dendritic cells. CD4 associates with major histocompatibility complex
CC (MHC) class II molecules on the surface of antigen presenting cells to
CC mediate efficient cellular immune response interactions. In humans CD4 is
CC the target of interaction with the human immunodeficiency virus HIV. The
CC immunoglobulin is used to kill cells infected with HIV, and for treating
CC or preventing infection. It is also used for imaging HIV-infected tissues
CC (for staging or prognosis of infection, and for assessing efficacy of
CC treatments). The immunoglobulin is also used to determine the HIV
CC envelope glycoprotein burden, once determined, this information is used
CC in the staging and prognosis of HIV infected patients. The
CC immunoglobulin should be active against all strains of HIV (since the
CC CD4-PR120 interaction is essential for infection). The heterotetramers
CC are assembled intracellularly and secreted efficiently from mammalian
CC cells, allowing high recovery and purification from the culture medium.
CC They have longer half-life in serum and greater avidity than heavy chain
CC dimers
XX
SQ Sequence 310 AA;

```

```

Db 61 ILGNQSFLLTKGPSKLNDRADSRRLWDQGNPFLIIKNLIKEDSDTYICEVEDQKEEVL 120
QY 121 LVFGLTANSDPHLLLOGSLTTLTSPGSSPSPVOCRRSPRGKNIQGGKTLTSLVQLQDSG 180
Db 121 LVFGLTANSDPHLLLOGSLTTLTSPGSSPSPVOCRRSPRGKNIQGGKTLTSLVQLQDSG 180
QY 181 TWTCTVLQNGKQKVEPKIDIVPPASALPAPPTGSALPDQOTASALPDPPAASALPALAVI 240
Db 181 TWTCTVLQNGKQKVEPKIDIVPAAFTVAAP-----SVFIPEPDEGLKSGTASV 228
QY 241 SFL 244
Db 229 VCLL 232

RESULT 5
AAB67324
ID AAB67324 standard; protein, 310 AA.
XX
AC AAB67324;
XX
DT 23-APR-2001 (first entry)
XX
DE CD4-kappa chimeric light chain protein.
XX
KM Immunoglobulin; chelator; chimeric; HIV; human immunodeficiency virus.
XX
OS Homo sapiens.
PN US6177549-B1.
XX
PD 23-JAN-2001.
XX
PF 10-JUN-1995; 99US-00329916.
XX
PR 07-AUG-1992; 92US-00927931.
PR 06-AUG-1993; 93WO-US007422.
PR 03-FEB-1995; 95US-00379516.
PR 07-JUN-1995; 95US-00477460.
XX
PA (PROG-) PROGENICS PHARM INC.
PI Maddon PJ, Allway GP;
XX
DR MPI; 2001-158582/16.
XX
PT Immunoglobulin for treating human immunodeficiency virus-infected
PT subject, consists of cytotoxic radionuclide linked to heterotetramer
PT comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-
PT kappalight chains.
XX
PS Disclosure; Fig 5; 43pp; English.
XX
CC The present invention relates to an immunoglobulin, comprising a
CC cytotoxic radionuclide linked, directly or via a bifunctional chelator,
CC to a heterotetramer having two chimeric CD4-IgG2 heavy chains encoded by
CC an expression vector CD4-IgG2HC-PRCMV and two chimeric CD4-kappa light
CC chains encoded by an expression vector CD4-KLC-PRCMV. The invention is
CC useful for killing human immunodeficiency virus (HIV)-infected cells, for
CC the treatment and prevention of infection with HIV
XX
SQ Sequence 310 AA;

```

Query Match 78.8%; Score 1038; DB 4; Length 310;  
 Best Local Similarity 85.7%; Pred. No. 2.8e-64;  
 Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

```

QY 1 MNRGVPFRLLLVLTQALLPAAQGNKVVYLGKGGDTVELTCTASOKKSIOFHKNSNQIK 60
Db 1 MNRGVPFRLLLVLTQALLPAAQGNKVVYLGKGGDTVELTCTASOKKSIOFHKNSNQIK 60
QY 61 ILGNQSFLLTKGPSKLNDRADSRRLWDQGNPFLIIKNLIKEDSDTYICEVEDQKEEVL 120

```

Db 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKI ESDTYICEVEQKEVQL 120  
 QY 121 LVFGLTANSPTHTLLQGQSLTLLTSPGSSPSVQCRSPRGKNIQGGKTLISVSOLELDGSG 180  
 Db 121 LVFGLTANSPTHTLLQGQSLTLLTSPGSSPSVQCRSPRGKNIQGGKTLISVSOLELDGSG 180  
 QY 181 TWCTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
 Db 181 TWCTCTVLQNKQKVEFKIDIVLAFTVAAP-----SVTFPPSDEQLKSGTASV 228  
 QY 241 SFLL 244  
 Db 229 VCLL 232

RESULT 6  
 AAB80885 standard; protein; 310 AA.  
 ID AAB80885;  
 AC AAB80885;  
 DT 29-MAY-2001 (first entry)  
 XX  
 XX Human CD4-kappa chimeric light chain.  
 DE Human, Anti-HIV, CD4-IgG2 chimeric heterotetramer;  
 KM Immunoglobulin gamma 2; CD4-kappa.  
 XX Homo sapiens.  
 OS  
 XX US6187748-B1.  
 PN 13-FEB-2001.  
 PD 07-JUN-1995; 95US-00485372.  
 PF 08-FEB-1991; 91US-00653684.  
 PR 10-FEB-1992; 92MO-US001143.  
 PR 08-DEC-1992; 92US-00960440.  
 XX  
 XX (PROG-) PROGENICS PHARM INC.  
 PA  
 XX Maddon PJ, Beaudry GA;  
 PI WPI; 2001-264981/27.  
 DR N-PSDB; AAF77831.  
 XX  
 XX Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell,  
 PT or treating a subject having CD4+ cells infected with HIV involves using  
 PT CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.  
 PS Disclosure; Fig 5; 55pp; English.  
 XX  
 XX The present invention relates to a method for inhibiting infection of a  
 CC CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2  
 CC chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of  
 CC glycoprotein 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface  
 CC protein that is expressed primarily on the surface of T cells. In  
 CC man, CD4 is the target of interaction with HIV. The heterotetramer has  
 CC two heavy and two light chains which are encoded by expression vectors  
 CC CD4-IgG2HC-PRCMV (V1) and CD4-kLC-PRCMV (V2), respectively. The method  
 CC is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+  
 CC cells of a subject from becoming infected with HIV. The method is also  
 CC useful for treating a subject having CD4+ cells infected with HIV. The  
 CC present sequence is human fusion protein: CD4-kappa chimeric light chain  
 CC of the CD4-IgG2 chimeric heterotetramer. This sequence was used in the  
 CC method of the present invention  
 XX  
 PS Sequence 310 AA;  
 SO

Query Match 78.8%; Score 1038; DB 4; Length 310;  
 Best Local Similarity 85.7%; Pred. No. 2.8e-64;  
 Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 MNRGVPFRHLVLVQLALLPAATQGNKVVLTGKKDVTVELTCTASOKKSTIOFHKNSNOIK 60  
 Db 1 MNRGVPFRHLVLVQLALLPAATQGNKVVLTGKKDVTVELTCTASOKKSTIOFHKNSNOIK 60  
 QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKI ESDTYICEVEQKEVQL 120  
 Db 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKI ESDTYICEVEQKEVQL 120  
 QY 121 LVFGLTANSPTHTLLQGQSLTLLTSPGSSPSVQCRSPRGKNIQGGKTLISVSOLELDGSG 180  
 Db 121 LVFGLTANSPTHTLLQGQSLTLLTSPGSSPSVQCRSPRGKNIQGGKTLISVSOLELDGSG 180  
 QY 181 TWCTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
 Db 181 TWCTCTVLQNKQKVEFKIDIVLAFTVAAP-----SVTFPPSDEQLKSGTASV 228  
 QY 241 SFLL 244  
 Db 229 VCLL 232

RESULT 7  
 ABG71124 standard; protein; 310 AA.  
 ID ABG71124;  
 AC ABG71124;  
 DT 17-JAN-2003 (first entry)  
 XX  
 XX CD4-kappa chimeric light chain of the CD4-IgG2 chimeric protein.  
 DE CD4, kappa light chain; human immunodeficiency virus-1, HIV-1, mutant;  
 KM mutein.  
 XX Homo sapiens.  
 OS  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FT Peptide 1..25  
 FT Protein /label= signal\_peptide 26..310  
 FT /note= "Mature CD4-kappa chimeric light chain of the CD4-IgG2 chimeric heterotetramer"  
 XX  
 XX US6451313-B1.  
 PN 17-SEP-2002.  
 PD 07-JUN-1995; 95US-00484681.  
 PF 08-FEB-1991; 91US-00653684.  
 PR 10-FEB-1992; 92MO-US001143.  
 PR 08-DEC-1992; 92US-00960440.  
 XX  
 XX (PROG-) PROGENICS PHARM INC.  
 PA  
 XX Maddon PJ, Beaudry GA;  
 PI WPI; 2003-038273/03.  
 DR N-PSDB; ABS55722.  
 XX  
 XX Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human  
 PT immunodeficiency virus-1 with two heavy and light chains encoded by  
 PT expression vectors designated CD4-IgG2HC-PRCMV and CD4-kLC-PRCMV,  
 PT respectively.  
 XX  
 PS Claim 1; Fig 5A-D; 54pp; English.  
 XX  
 XX The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric  
 CC heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-  
 CC 1) having two heavy chains encoded by an expression vector designated CD4  
 CC -IgG2HC-PRCMV, and two light chains encoded by expression vector

CC designated CD4-KLc-PRCCMV. (I) and a composition (II) comprising (I) or  
 CC (1) linked to a toxin, are useful for inhibiting HIV infection of a CD4  
 CC cell, and preventing a subject being infected with HIV by blocking the  
 CC spread of HIV infection. This is the amino acid sequence of the CD4-kappa  
 CC chimeric light chain of the CD4-IgG2 chimeric heterotetramer useful in  
 CC inhibiting HIV infection

XX Sequence 310 AA:

Query Match 78.8%; Score 1038; DB 6; Length 310;  
 Best Local Similarity 85.7%; Pred. No. 2.8e-64;  
 Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 MNRGVPFRLHLIVLQALLPAAATQGNKVVYLGKKGDTVELTCTASQKSIQFMKNSNQIK 60  
 DB 1 MNRGVPFRLHLIVLQALLPAAATQGNKVVYLGKKGDTVELTCTASQKSIQFMKNSNQIK 60  
 QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEYVL 120  
 DB 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEYVL 120  
 QY 121 LVFGTLTANSPTHTLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGTLTANSPTHTLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 QY 181 TWCTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPPPPASALPALAVI 240  
 DB 181 TWCTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPPPPASALPALAVI 240  
 QY 241 SFLL 244  
 DB 229 VCLL 232

RESULT 8  
 ID AAE37574 standard; protein; 450 AA.  
 AC AAE37574;

DT 27-AUG-2003 (first entry)

DE Human D1D2-Ig alphacp fusion protein.

KM Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig;  
 KM human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; D1;  
 KM D2; alpha tailpiece; alphacp; fusion protein.

OS Homo sapiens.

PN WO2003040311-A2.

PD 15-MAY-2003.

PF 24-OCT-2002; 2002WO-US034393.

PR 25-OCT-2001; 2001US-0346231P.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Archos J, Cicala C, Fauci AS;

DR WPI; 2003-441545/41.

DR N-PSDB; AAD29113.

PT New CD4 polypeptide ligated at its C-terminus with a portion of an  
 PT immunoglobulin, useful for preparing a composition for treating or  
 PT preventing HIV-1 infection.

PS Example 1; Page 47; 100pp; English.

CC The invention relates to a CD4 (cluster of differentiation factor 4)  
 CC polypeptide ligated at its C-terminus with a portion of an immunoglobulin

CC (Ig) comprising a hinge region and a constant domain of a mammalian Ig  
 CC heavy chain. The polypeptide comprises a tailpiece from the C-terminus of  
 CC the heavy chain of an IGA or IGM antibody. Polypeptides of the invention  
 CC are useful for preparing a composition for treating or preventing human  
 CC immunodeficiency virus (HIV)-1 infection. The invention is useful in gene  
 CC therapy and also in the preparation of vaccines. The present sequence is  
 CC a fusion protein which comprises a human IgA alpha tailpiece (alphatp), a  
 CC human IGG constant region comprising a hinge, a CH2 and CH3 region and a  
 CC human CD4 D1D2 domain

XX Sequence 450 AA:

Query Match 78.7%; Score 1036.5; DB 6; Length 450;  
 Best Local Similarity 89.7%; Pred. No. 5.5e-64;  
 Matches 208; Conservative 0; Mismatches 19; Indels 5; Gaps 1;

QY 1 MNRGVPFRLHLIVLQALLPAAATQGNKVVYLGKKGDTVELTCTASQKSIQFMKNSNQIK 60  
 DB 1 MNRGVPFRLHLIVLQALLPAAATQGNKVVYLGKKGDTVELTCTASQKSIQFMKNSNQIK 60  
 QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEYVL 120  
 DB 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEYVL 120  
 QY 121 LVFGTLTANSPTHTLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGTLTANSPTHTLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 QY 181 TWCTCTVLQNKQKVEFKIDIVPRASA-----LPAPPTGSALPDPQTASALPDP 227  
 DB 181 TWCTCTVLQNKQKVEFKIDIVPRASA-----LPAPPTGSALPDPQTASALPDP 227

RESULT 9  
 ID AAR26531 standard; protein; 534 AA.  
 AC AAR26531;

DT 25-MAR-2003 (revised)  
 DT 28-JAN-1993 (first entry)

DE Sequence of CD4-IgG1 chimeric heavy chain heterotetramer.

KM CD4-gamma 1 chimeric heavy chain homodimer; expression vector; HIV;  
 KM therapy; diagnostic agent; inhibition.

OS Synthetic.

PN WO9213559-A1.

PD 20-AUG-1992.

PF 10-FEB-1992; 92WO-US001152.

PR 08-FEB-1991; 91US-00654205.

PA (PROG-) PROGENICS PHARM INC.

PI Beaudry GA, Madden PJ;

DR WPI; 1992-299758/36.

DR N-PSDB; AAO27831.

PT

PT

PS

CC

CC

```
XX CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector -
PT for preventing and creating HIV infection useful as a diagnostic agent.
XX
XX Example; Fig 4; 89pp; English.
XX
CC The human CD4 cDNA is excised from the plasmid pSP6T4 and cloned into
CC M13mp18. In order to excise a fragment containing the CH1 exon of the
CC human gamma 1 heavy chain gene, the plasmid pSP gamma 1 is digested with
CC SacII, and the SacII sites are then made flush using T4 DNA polymerase.
CC The fragment containing the CH1 exon is then purified and ligated to the
CC M13mp18(CD4) vector. Oligonucleotide-mediated site-directed mutagenesis
CC is then performed to juxtapose the CD4 and CH1 sequences in frame. The
CC CD4-CH1 chimeric gene is then linearized and ligated to the pSP6T4 DNA
CC fragment of the plasmid pSP gamma 1 containing the hinge, CH2, and CH3
CC exons of the human gamma 1 chain gene designated CD4-IgG1HC-pSP6T4 (ATCC
CC 75192). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 534 AA;
Query Match 78.4%; Score 1033; DB 2; Length 534;
Best Local Similarity 85.7%; Pred. No. 1.2e-63;
Matches 209; Conservative 3; Mismatches 10; Indels 22; Gaps 3;
QY 1 MNRGVPRHLLVQLALPAAATQGNKVVGGKGDVLTCTASOKKSIQFHKNSNQIK 60
DB 1 MNRGVPRHLLVQLALPAAATQGNKVVGGKGDVLTCTASOKKSIQFHKNSNQIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLITKNIKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLITKNIKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPDTHLQGSGLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPDTHLQGSGLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVQNOQKVEFKIDIVLAFASTKGPSVFPPLAPSSKSTSGGTAALGLVKDYFPEP 240
DB 181 TWTCTVQNOQKVEFKIDIVLAFASTKGPSVFPPLAPSSKSTSGGTAALGLVKDYFPEP 240
QY 219 QTAS 222
DB 241 VTVS 244
RESULT 10
AAR26782
ID AAR26782 standard; protein; 432 AA.
XX
AC AAR26782;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 06-FEB-1993 (first entry)
XX
DE CD4-gamma2 chimeric heavy chain homodimer.
XX
KW homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
KW chimeric; increased serum half life; HIV infection; AIDS; ss.
XX
OS Homo sapiens.
OS Chimeric.
XX
FH Key
FH Domain 1. .216
FH Domain /label= CD4
FH Domain 217. 325
FH Domain /label= CH2
FH Domain 326. 433
FH Domain /label= CH3
XX
XX MO9213947-A1.
```

```
PD 20-AUG-1992.
XX
XX 10-FEB-1992; 92MO-US001143.
XX
XX 08-FEB-1991; 91US-00653684.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
XX Beaudry GA, Maddon PJ;
XX WPI; 1992-300034/36.
XX DR N-PSDB; AAQ28088.
XX
PT CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
PT treatment, prevention and diagnosis of HIV infection.
XX
XX Claim 2; Fig 3; 90pp; English.
XX
CC This sequence represents a CD4-gamma2 chimeric heavy chain homodimer. It
CC was produced by expression of the coding mutagenised cDNA (produced as
CC described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently
CC assembled intracellularly and effectively secreted from mammalian cells
CC pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery
CC and purification from the medium of cells expressing it. It possesses
CC increased serum half-life and has increased avidity for HIV cf. heavy
CC chain dimers. It can inhibit HIV infection of CD4+ cells and block the
CC spread of HIV infection within a patient. Attachment to a detectable
CC marker makes it useful in an assay for HIV or SIV infection, and it can
CC also be linked to toxins, eg diphtheria, pseudomonas exotoxin A (domains
CC I or II) or the deoxycoylated A-chain of ricin. (Updated on 25-MAR-2003
CC to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 432 AA;
Query Match 78.4%; Score 1032.5; DB 2; Length 432;
Best Local Similarity 88.0%; Pred. No. 9.9e-64;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;
QY 1 MNRGVPRHLLVQLALPAAATQGNKVVGGKGDVLTCTASOKKSIQFHKNSNQIK 60
DB 1 MNRGVPRHLLVQLALPAAATQGNKVVGGKGDVLTCTASOKKSIQFHKNSNQIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLITKNIKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLITKNIKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPDTHLQGSGLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPDTHLQGSGLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVQNOQKVEFKIDIVLAFASTKGPSVFPPLAPSSKSTSGGTAALGLVKDYFPEP 240
DB 181 TWTCTVQNOQKVEFKIDIVLAFASTKGPSVFPPLAPSSKSTSGGTAALGLVKDYFPEP 240
RESULT 11
AAR46678
ID AAR46678 standard; protein; 432 AA.
XX
AC AAR46678;
XX
DT 25-MAR-2003 (revised)
DT 08-AUG-1994 (first entry)
XX
DE CD4-gamma 2 chimeric heavy chain.
XX
KW CD4; gamma; heavy chain; chimeric; chimeric; immunocjugate; HIV;
KW human immunodeficiency virus; radionuclide; toxin; therapy; treatment;
KW imaging; detection; targeting.
XX
XX Homo sapiens.
XX
XX Key
XX Location/Qualifiers
```









CC the spread of HIV infection within a patient. Attachment to a detectable  
 CC marker makes it useful in an assay for HIV or SIV infection, and it can  
 CC also be linked to toxins, eg Diphtheria, Pseudomonas exotoxin A (domains  
 CC I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003  
 CC to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)

XX Sequence 530 AA;

Query Match 78.2%; Score 1030.5; DB 2; Length 530;

Best Local Similarity 84.8%; Pred. No. 1,7e-63;

Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPRHLLVLTQALPPATQGNKVLGKGGDTVELCTASQKKSIOFHMKNSNOIK 60

DB 1 MNRGVPRHLLVLTQALPPATQGNKVLGKGGDTVELCTASQKKSIOFHMKNSNOIK 60

QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120

DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120

QY 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLELDQSG 180

DB 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLELDQSG 180

QY 181 TWTCTVLQNGKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPALAVI 240

DB 181 TWTCTVLQNGKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPALAVI 240

QY 241 SFL 244

DB 230 GCLV 233

RESULT 17

AAV85080 ID AAV85080 standard; protein; 530 AA.

XX AAV85080;

DT 19-JUN-2000 (first entry)

DE CD4-IgG2 chimeric heterotetramer heavy chain amino acid sequence.

KM CD4-IgG2 chimeric heavy chain heterotetramer; immunocjugate; treatment;

KM cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;

KM cellular immune response interaction mediator; HIV interaction; staging;

XX prognosis; envelope glycoprotein burden; human.

OS Homo sapiens.

XX US6034223-A.

PD 07-MAR-2000.

PF 07-JUN-1995; 95US-00477460.

PR 07-AUG-1992; 92US-00927931.

PR 06-AUG-1993; 93WO-US007422.

PR 03-FEB-1995; 95US-00379516.

XX (PROG-) PROGENICS PHARM INC.

PI Allaway GP, Maddon PJ;

DR WPI; 2000-269502/23.

DR N-PSDB; AA298856.

XX New immunocjugate, used to treat, prevent or image human immune

PT deficiency virus infection, comprises radionuclide attached to

PT heterotetramer of CD4-immunoglobulin chimeras.

XX Disclosure; Fig 4; 58pb; English.

CC This sequence represents the CD4-IgG2 chimeric heavy chain amino acid  
 CC sequence from the CD4-IgG2 chimeric heterotetramer. The invention relates  
 CC to an immunocjugate comprising a cytotoxic radionuclide and a  
 CC heterotetramer of two heavy chains and two light chains. The cytotoxic  
 CC radionuclide is linked to either the heavy chains or the light chains, or  
 CC to all four chains, directly or through a bifunctional chelator. Both  
 CC heavy chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by  
 CC vector CD4-IgG2HC-PRCMV (ATCC 75193) and both light chains are chimeric  
 CC CD4-kappa chains encoded by vector CD4-kLC-pRCMV (ATCC 75194). CD4 is a  
 CC non-polymorphic cell surface glycoprotein that is expressed on the  
 CC surface of helper T lymphocytes, cells of the monocyte/macrophage lineage  
 CC and dendritic cells. CD4 associates with major histocompatibility complex  
 CC (MHC) class II molecules on the surface of antigen presenting cells to  
 CC mediate efficient cellular immune response interactions. In humans CD4 is  
 CC the target of interaction with the human immunodeficiency virus HIV. The  
 CC immunocjugate is used to kill cells infected with HIV, and for treating  
 CC or preventing infection. It is also used for imaging HIV-infected tissues  
 CC (for staging or prognosis of infection, and for assessing efficacy of  
 CC treatments). The immunocjugate is also used to determine the HIV  
 CC envelope glycoprotein burden, once determined, this information is used  
 CC in the staging and prognosis of HIV infected patients. The  
 CC immunocjugate should be active against all strains of HIV (since the  
 CC CD4-gp120 interaction is essential for infection). The heterotetramers  
 CC are assembled intracellularly and secreted efficiently from mammalian  
 CC cells, allowing high recovery and purification from the culture medium.  
 CC They have longer half-life in serum and greater avidity than heavy chain  
 CC dimers

XX Sequence 530 AA;

Query Match 78.2%; Score 1030.5; DB 3; Length 530;

Best Local Similarity 84.8%; Pred. No. 1,7e-63;

Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPRHLLVLTQALPPATQGNKVLGKGGDTVELCTASQKKSIOFHMKNSNOIK 60

DB 1 MNRGVPRHLLVLTQALPPATQGNKVLGKGGDTVELCTASQKKSIOFHMKNSNOIK 60

QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120

DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120

QY 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLELDQSG 180

DB 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLELDQSG 180

QY 181 TWTCTVLQNGKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPALAVI 240

DB 181 TWTCTVLQNGKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPPAASALPALAVI 240

QY 241 SFL 244

DB 230 GCLV 233

RESULT 18

AAV87323 ID AAV87323 standard; protein; 530 AA.

XX AAV87323;

DT 23-APR-2001 (first entry)

DE CD4-IgG2 chimeric heavy chain protein.

KM Immunocjugate; chelator; chimeric; HIV; human immunodeficiency virus.

KM Homo sapiens.

XX US6177549-B1.

XX 23-JAN-2001.

PF 10-JUN-1999; 99US-00329916.  
XX  
XX 07-AUG-1992; 92US-00927931.  
PR 06-AUG-1993; 93MO-US007422.  
PR 03-FEB-1995; 95US-00379516.  
PR 07-JUN-1995; 95US-00477460.  
XX  
XX (PROG-) PROGENICS PHARM INC.  
XX  
XX Maddon PJ, Allaway GP;  
XX  
XX WPI, 2001-158582/16.  
XX  
XX Immunodeficiency for treating human immunodeficiency virus-infected  
PT subject, consists of cytotoxic radionuclide linked to heterotetramer  
PT comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-  
PT kappa1 light chains.  
XX  
XX Disclosure; Fig 4; 43pp; English.  
XX  
XX The present invention relates to an immunoconjugate, comprising a  
CC cytotoxic radionuclide linked, directly or via a bifunctional chelator,  
CC to a heterotetramer having two chimeric CD4-IgG2 heavy chains encoded by  
CC an expression vector CD4-IgG2HC-PRCMV and two chimeric CD4-kappa 1 light  
CC chains encoded by an expression vector CD4-kLC-PRCMV. The invention is  
CC useful for killing human immunodeficiency virus (HIV)-infected cells, for  
CC the treatment and prevention of infection with HIV  
XX  
XX Sequence 530 AA;  
SQ  
Query Match 78.2%; Score 1030.5; DB 4; Length 530;  
Best Local Similarity 84.8%; Pred. No. 1.7e-63;  
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;  
QY 1 MNRGVPFRLLLVLTOLALPPATQGNKVTGKGGDTVELTCTASQKKSIOFHKNSNOIK 60  
DB 1 MNRGVPFRLLLVLTOLALPPATQGNKVTGKGGDTVELTCTASQKKSIOFHKNSNOIK 60  
QY 61 ILNGSGFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLKIETSDPTVYICEVEDQKEVOL 120  
DB 61 ILNGSGFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLKIETSDPTVYICEVEDQKEVOL 120  
QY 121 LVFGLTANSPTHLQGGOSTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDGSG 180  
DB 121 LVFGLTANSPTHLQGGOSTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDGSG 180  
QY 181 TWTCTVLQNOQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240  
DB 181 TWTCTVLQNOQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240  
QY 241 SFL 244  
DB 230 GCLV 233  
RESULT 19  
ID AAB80884 standard; protein; 530 AA.  
XX  
XX AAB80884;  
XX  
XX 29-MAY-2001 (first entry)  
XX  
XX Human CD4-IgG2 chimeric heavy chain.  
DE  
XX Human; Anti-HIV; CD4-IgG2 chimeric heterotetramer;  
KW Immunoglobulin gamma 2.  
XX  
XX Homo sapiens.  
OS  
XX US6187748-B1.  
PN  
XX 13-FEB-2001.  
PD

XX  
XX 07-JUN-1995; 95US-00485372.  
XX  
XX 08-FEB-1991; 91US-00653664.  
PR 10-FEB-1992; 92MO-US001143.  
PR 08-DEC-1992; 92US-00960440.  
XX  
XX (PROG-) PROGENICS PHARM INC.  
XX  
XX Maddon PJ, Beaudry GA;  
XX  
XX WPI, 2001-264981/27.  
DR N-PSDB; AAF77830.  
XX  
XX Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell,  
PT or treating a subject having CD4+ cells infected with HIV involves using  
PT CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.  
XX  
XX Disclosure; Fig 4; 55pp; English.  
XX  
XX The present invention relates to a method for inhibiting infection of a  
CC CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2  
CC chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of  
CC differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface  
CC glycoprotein that is expressed primarily on the surface of T cells. In  
CC man, CD4 is the target of interaction with HIV. The heterotetramer has  
CC two heavy and two light chains which are encoded by expression vectors  
CC CD4-IgG2HC-PRCMV (VI) and CD4-kLC-PRCMV (V2), respectively. The method  
CC is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+  
CC cells of a subject from becoming infected with HIV. The method is also  
CC useful for treating a subject having CD4+ cells infected with HIV. The  
CC present sequence is human fusion protein: CD4-Ig2 chimeric heavy chain of  
CC the CD4-Ig2 chimeric heterotetramer. This sequence was used in the  
CC method of the present invention  
XX  
XX Sequence 530 AA;  
SQ  
Query Match 78.2%; Score 1030.5; DB 4; Length 530;  
Best Local Similarity 84.8%; Pred. No. 1.7e-63;  
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;  
QY 1 MNRGVPFRLLLVLTOLALPPATQGNKVTGKGGDTVELTCTASQKKSIOFHKNSNOIK 60  
DB 1 MNRGVPFRLLLVLTOLALPPATQGNKVTGKGGDTVELTCTASQKKSIOFHKNSNOIK 60  
QY 61 ILNGSGFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLKIETSDPTVYICEVEDQKEVOL 120  
DB 61 ILNGSGFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLKIETSDPTVYICEVEDQKEVOL 120  
QY 121 LVFGLTANSPTHLQGGOSTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDGSG 180  
DB 121 LVFGLTANSPTHLQGGOSTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDGSG 180  
QY 181 TWTCTVLQNOQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240  
DB 181 TWTCTVLQNOQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240  
QY 241 SFL 244  
DB 230 GCLV 233  
RESULT 20  
ID ABG71123 standard; protein; 530 AA.  
XX  
XX ABG71123;  
XX  
XX 17-JAN-2003 (first entry)  
XX  
XX CD4-immunoglobulin G2 (IgG2) chimeric heterotetramer.  
DE  
XX CD4; immunoglobulin G2; Ig gamma2; human immunodeficiency virus-1; HIV-1;  
KW

KM mutant; mutein.  
XX Homo sapiens.  
OS Synthetic.  
XX

Location/Qualifiers  
1..25  
/label=Signal\_peptide

FT Peptide  
FT Protein  
/note="Mature CD4-IgG2 chimeric heterotetramer"

XX US6451313-B1.

XX 17-SEP-2002.

XX 07-JUN-1995; 95US-00484681.

XX 08-FEB-1991; 91US-00653684.

PR 10-FEB-1992; 92WO-US001143.

PR 08-DEC-1992; 92US-00960440.

XX (PROG-) PROGENICS PHARM INC.

XX Maddon PJ, Beaudry GA;

XX WPI; 2003-038273/03.

DR N-PSDB; ABS55721.

XX Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human immunodeficiency virus-1 with two heavy and light chains encoded by expression vectors designated CD4-IgG2HC-prcCMV and CD4-KLC-prcCMV, respectively.

XX Claim 1; Fig 4A-H; 54pp; English.

XX The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric heterotetramer (I) that neutralizes human immunodeficiency virus-1 (HIV-1) having two heavy chains encoded by an expression vector designated CD4-IgG2HC-prcCMV, and two light chains encoded by expression vector designated CD4-KLC-prcCMV. (II) and a composition (III) comprising (I) or (II) linked to a toxin, are useful for inhibiting HIV infection of a CD4 cell, and preventing a subject being infected with HIV by blocking the spread of HIV infection. This is the amino acid sequence of the CD4-immunoglobulin G2 chimeric heavy chain chimeric heterotetramer useful in inhibiting HIV infection

XX Sequence 530 AA;

Query Match 78.2%; Score 1030.5; DB 6; Length 530;

Best Local Similarity 84.8%; Pred. No. 1,7e-63; Mismatches 21; Indels 11; Gaps 1;

Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVFRRHLLLVQLALPAATQGNKRVLGKKGDTVELTCTASOKKSIQFHKNSNOIK 60

DB 1 MNRGVFRRHLLLVQLALPAATQGNKRVLGKKGDTVELTCTASOKKSIQFHKNSNOIK 60

QY 61 ILGNQGSFLLTKGSKLNDRAADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQL 120

DB 61 ILGNQGSFLLTKGSKLNDRAADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQL 120

QY 121 LVFGLTANSDBTHLLQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLDLQDSG 180

DB 121 LVFGLTANSDBTHLLQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLDLQDSG 180

QY 181 TWCTCTVLQONQKVEFKIDIVPRASALPDPGTASALPDPPAASALPALAVI 240

DB 181 TWCTCTVLQONQKVEFKIDIVPRASALPDPGTASALPDPPAASALPALAVI 240

QY 241 SFLL 244

DB 230 GCLV 233

RESULT 21

AAR78674

XX AAR78674 standard; protein; 203 AA.

AC AAR78674;

DT 12-APR-1996 (first entry)

XX CD4 domains D1-D2.

XX Chimeric receptor; CD4, T-cell receptor; HIV; cytolysis;

XX human immunodeficiency virus; adoptive immunotherapy.

OS Homo sapiens.

XX W09521528-A1.

XX 17-AUG-1995.

XX 12-JAN-1995; 95WO-US000454.

XX 14-FEB-1994; 94US-00195395.

PR 02-AUG-1994; 94US-00284391.

XX (GEHO ) GEN HOSPITAL CORP.

XX Seed B, Banapour B, Romeo C, Kolanus W;

XX WPI; 1995-292893/38.

DR N-PSDB; AAC96104.

XX Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing cells.

XX Example 10; Fig 24; 118pp; English.

XX Extracellular domains D1-D4 (AAR78673) or D1-D2 (AAR78674) of human CD4

XX are used in the construction of chimeric receptors utilised in the

XX targeted cytolysis of cells expressing HIV envelope proteins on their

XX surface. The chimeric receptors comprise the extracellular domain (pref.

XX amino acids 1-394 or 1-200) of CD4 linked to an intracellular portion,

XX e.g. of T-cell receptor protein zeta

XX Sequence 203 AA;

Query Match 78.1%; Score 1029; DB 2; Length 203;

Best Local Similarity 100.0%; Pred. No. 7.5e-64; Mismatches 0; Indels 0; Gaps 0;

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVFRRHLLLVQLALPAATQGNKRVLGKKGDTVELTCTASOKKSIQFHKNSNOIK 60

DB 1 MNRGVFRRHLLLVQLALPAATQGNKRVLGKKGDTVELTCTASOKKSIQFHKNSNOIK 60

QY 61 ILGNQGSFLLTKGSKLNDRAADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQL 120

DB 61 ILGNQGSFLLTKGSKLNDRAADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQL 120

QY 121 LVFGLTANSDBTHLLQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLDLQDSG 180

DB 121 LVFGLTANSDBTHLLQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLDLQDSG 180

QY 181 TWCTCTVLQONQKVEFKIDIV 200

DB 181 TWCTCTVLQONQKVEFKIDIV 200

RESULT 22

AAR89451

XX AAR89451 standard; peptide; 203 AA.

AC AAR89451;

DT 26-SEP-1996 (first entry)

```
XX CD4 D1-D2 domains.
DE
XX
XX CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IGL;
KM human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
KM dendritic cell; therapy; mammal; infection.
OS
XX Homo sapiens.
XX MO9603863-A1.
PN
XX 15-FEB-1996.
PD
XX 26-JUL-1995; 95MO-US009468.
PF
XX 02-AUG-1994; 94US-00284391.
PR 24-FEB-1995; 95US-00394388.
XX
XX (GEHO ) GEN HOSPITAL CORP.
PA
XX Seed B, Banapour B, Romeo C, Kolanus W;
PI
XX WPI; 1996-129034/13.
DR N-PSDB; AAT10738.
XX
XX Membrane-bound chimeric receptor comprising extracellular portion
PT including CD4 fragment - cells expressing receptor can be used for
PT treatment of HIV infection.
XX
XX Example 10; Fig 24; 134pp; English.
XX
XX This sequence represents the CD4 D1-D2 domains of CD4. This sequence is
CC included in the membrane bound proteinaceous chimeric receptor of the
CC invention. The extracellular portion of the chimeric receptor contains a
CC fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence) which
CC specifically recognises and binds HIV-infected cells, but does not
CC mediate HIV infection. The extracellular domain of the receptor is
CC separated from the cell membrane by 48 or 72 angstroms, or by one or more
CC proteinaceous alpha-helices. The transmembrane region of the chimeric
CC receptor contains a portion of the CD7, CD5 or CD34 transmembrane domain.
CC Alternatively, the extracellular portion of the receptor can also be
CC separated from the intracellular domain by the hinge, CH2 and CH3 domains
CC of human IgL. The cells expressing the receptor are preferably T cells,
CC B cells, neutrophils, or dendritic cells. The therapeutic cells
CC expressing the chimeric receptor are administered to a mammal to treat
CC HIV infection
CC
XX
XX Sequence 203 AA;
SQ
Query Match 78.1%; Score 1029; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.5e-64;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPRFRLHLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
DB 1 MNRGVPRFRLHLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
QY 61 ILGNQGSFLLTKGSPSKLMDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQGSFLLTKGSPSKLMDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
QY 121 LVFGLTANSPTHLLOQGSLLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSLLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNOQKVEFKIDIV 200
DB 181 TWTCTVLQNOQKVEFKIDIV 200
```

RESULT 23  
AAR78673  
ID AAR78673 standard; protein; 398 AA.

```
XX AAR78673;
AC
XX 12-APR-1996 (first entry)
DT
XX CD4 domain D1-D4.
DE
XX
XX Chimeric receptor; CD4; T-cell receptor; HIV; cytolysis;
KM human immunodeficiency virus; adoptive immunotherapy.
XX
XX Homo sapiens.
OS
XX WO9521528-A1.
PN
XX 17-AUG-1995.
PD
XX 12-JAN-1995; 95MO-US000454.
PF
XX 14-FEB-1994; 94US-00195395.
PR 02-AUG-1994; 94US-00284391.
XX
XX (GEHO ) GEN HOSPITAL CORP.
PA
XX Seed B, Banapour B, Romeo C, Kolanus W;
PI
XX WPI; 1995-292893/38.
DR N-PSDB; AAG96103.
XX
XX Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing
PT cells.
PT
XX
XX Example 10; Fig 23; 118pp; English.
XX
XX Extracellular domain D1-D4 (AAR78673) or D1-D2 (AAR78674) of human CD4
CC are used in the construction of chimeric receptors utilised in the
CC targeted cytolysis of cells expressing HIV envelope proteins on their
CC surface. The chimeric receptors comprise the extracellular domain (pref.
CC amino acids 1-394 or 1-200) of CD4 linked to an intracellular portion,
CC e.g. of T-cell receptor protein zeta
CC
XX
XX Sequence 398 AA;
SQ
Query Match 78.1%; Score 1029; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.6e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPRFRLHLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
DB 1 MNRGVPRFRLHLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
QY 61 ILGNQGSFLLTKGSPSKLMDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQGSFLLTKGSPSKLMDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
QY 121 LVFGLTANSPTHLLOQGSLLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSLLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNOQKVEFKIDIV 200
DB 181 TWTCTVLQNOQKVEFKIDIV 200
```

RESULT 24  
AAR89450  
ID AAR89450 standard; peptide; 398 AA.  
AC AAR89450;  
XX  
XX 26-SEP-1996 (first entry)  
DT  
XX CD4 D1-D4 domains.  
DE  
XX

KM CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1;  
 KM human; CD4; HIV; proteoglycan alpha-helix; T cell; B cell; neutrophil;  
 KM dendritic cell; therapy; mammal; infection.  
 OS Homo sapiens.  
 XX MO9603883-A1.  
 XX PN  
 XX 15-FEB-1996.  
 PD  
 XX 26-JUL-1995; 95MO-US009468.  
 PF  
 XX 02-AUG-1994; 94US-00284391.  
 PR 24-FEB-1995; 95US-00394388.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 XX Seed B, Banapour B, Romeo C, Kolanus W;  
 PI  
 XX WPI; 1996-129034/13.  
 DR N-PSDB; AAT10797.  
 DR  
 XX  
 XX Membrane-bound chimeric receptor comprising extracellular portion  
 PT including CD4 fragment - cells expressing receptor can be used for  
 treatment of HIV infection.  
 XX  
 XX Example 10; Fig 23; 134pp; English.  
 PS  
 XX This sequence represents the D1-D4 domains of CD4. This sequence is  
 CC included in the membrane bound proteoglycan chimeric receptor of the  
 CC invention. The extracellular portion of the chimeric receptor contains a  
 CC fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence) which  
 CC specifically recognises and binds HIV-infected cells, but does not  
 CC mediate HIV infection. The extracellular domain of the receptor is  
 CC separated from the cell membrane by 48 or 72 angstroms, or by one or more  
 CC proteoglycan alpha-helices. The transmembrane region of the chimeric  
 CC receptor contains a portion of the CD7, CD5 or CD34 transmembrane domain.  
 CC Alternatively, the extracellular portion of the receptor can also be  
 CC separated from the intracellular domain by the hinge, CH2 and CH3 domains  
 CC of human IgG1. The cells expressing the receptor are preferably T cells,  
 CC B cells, neutrophils, or dendritic cells. The therapeutic cells  
 CC expressing the chimeric receptor are administered to a mammal to treat  
 CC HIV infection  
 CC  
 XX Sequence 398 AA;  
 SQ  
 Query Match 78.1%; Score 1029; DB 2; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-63;  
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNRGVPRHLLVLTQALPAATQGNKVVLGKKDVTVELTCTASQKKSIOFHMKNSQIK 60  
 DB 1 MNRGVPRHLLVLTQALPAATQGNKVVLGKKDVTVELTCTASQKKSIOFHMKNSQIK 60  
 QY 61 ILGNQGSFLLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEDQKEVOL 120  
 DB 61 ILGNQGSFLLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEDQKEVOL 120  
 QY 121 LVFGLTANSPTHLTLOGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLSSVQLELQDSG 180  
 DB 121 LVFGLTANSPTHLTLOGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLSSVQLELQDSG 180  
 QY 181 TWTCTVLTQNKQKVEFKIDIV 200  
 DB 181 TWTCTVLTQNKQKVEFKIDIV 200  
 RESULT 25  
 AAR06374 standard; protein; 400 AA.  
 ID AAR06374  
 XX AAR06374;  
 AC  
 XX  
 XX

DT 31-OCT-2002 (revised)  
 DT 20-DEC-1990 (first entry)  
 XX  
 XX Truncated form of soluble T4 encoded by PBG381.  
 DE  
 XX plasmid PBG381; soluble T4 protein; AIDS; ARC; HIV.  
 KM  
 XX  
 XX Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..23  
 FT /label= secretory signal  
 FT /note= "hydrophobic"  
 FT Region 24..117  
 FT /label= extracellular  
 FT /note= "homology to V-regions"  
 FT Region 118..132  
 FT /label= extracellular  
 FT /note= "homology to J-regions"  
 FT Region 133..397  
 FT /label= extracellular  
 FT /note= "glycosylated"  
 FT  
 XX MO9008198-A.  
 XX  
 XX 26-JUL-1990.  
 PD  
 XX 18-JAN-1989; 89US-00300096.  
 PF  
 XX 18-JAN-1989; 89US-00300096.  
 PR 18-JAN-1989; 89US-00300096.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 PI Letvin NA;  
 XX  
 XX WPI; 1990-254040/33.  
 DR N-PSDB; AAQ05608.  
 DR  
 XX  
 XX Treating or preventing AIDS, ARC or HIV infection - by administering an  
 PT immunologically effective amt. of soluble T4 protein.  
 PT  
 PS Disclosure; Fig 2; 121pp; English.  
 CC  
 XX T4-encoding plasmid PBG381 was used to transform Chinese Hamster Ovary  
 CC cells for the production of truncated T4. Soluble T4 is produced by  
 CC virtue of the removal of the transmembrane and cytoplasmic domains. The  
 CC soluble forms may be modified to increase their immunogenicity by  
 CC addition of an adjuvant such as incomplete Freund's adjuvant. The T4  
 CC interferes with HIV/T4 interaction and elicits anti-soluble T4 antibody  
 CC production. See also AAQ05607. (Updated on 31-OCT-2002 to add missing OS  
 CC field.)  
 CC  
 XX Sequence 400 AA;  
 SQ  
 Query Match 78.1%; Score 1029; DB 2; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-63;  
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNRGVPRHLLVLTQALPAATQGNKVVLGKKDVTVELTCTASQKKSIOFHMKNSQIK 60  
 DB 1 MNRGVPRHLLVLTQALPAATQGNKVVLGKKDVTVELTCTASQKKSIOFHMKNSQIK 60  
 QY 61 ILGNQGSFLLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEDQKEVOL 120  
 DB 61 ILGNQGSFLLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEDQKEVOL 120  
 QY 121 LVFGLTANSPTHLTLOGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLSSVQLELQDSG 180  
 DB 121 LVFGLTANSPTHLTLOGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLSSVQLELQDSG 180  
 QY 181 TWTCTVLTQNKQKVEFKIDIV 200  
 DB 181 TWTCTVLTQNKQKVEFKIDIV 200

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RESULT 26
AAP91922
ID AAP91922 standard; protein; 402 AA.
XX
AC AAP91922;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 14-MAY-1990 (first entry)
XX
DE Sequence of a secreted form of the CD4 adhesion (CD4T) polypeptide.
XX
KM CD4 variants; CD4T, gp120, plasmid pRCD4, HIV-1, HTLV-IIIB.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 25..26 /note="signal processing site"
FT Misc-difference 366 /note="other forms of CD4T terminate here"
FT Misc-difference 368 /note="other forms of CD4T terminate here"
FT Misc-difference /note="other forms of CD4T terminate here"
XX
PN BP314317-A.
XX
PD 03-MAY-1989.
XX
PF 03-OCT-1988; 88EP-00309194.
XX
PR 02-OCT-1987; 87US-00104329.
PR 28-SEP-1988; 88US-00250785.
XX
PA (GENTH ) GENENTECH INC.
XX
PI Capon DJ, Gregory TJ;
XX
DR WPI; 1989-111855/18.
DR N-PSDB; AAN90777.
XX
PT Compens. contg. adhesion variants - useful in therapy and diagnostics,
PT e.g. CD4 variants which are therapeutically useful for treating human
PT immuno-deficiency virus.
XX
PS Disclosure; Fig 1a-1c; 36pp; English.
XX
CC It may be capable of binding gp120. It may be fused with an
CC immunoglobulin constant domain, human transferrin, apolipoprotein,
CC albumin, ricin A chain or diphtheria toxin A. It may be used for
CC antiviral of immunomodulatory therapy particularly in treatment of HIV
CC infection. It may have variants by insertion, substitution of deletion in
CC non-functional regions. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 402 AA;
XX
Query Match 78.1%; Score 1029; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.6e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIQPHKNSNOIK 60
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIQPHKNSNOIK 60
QY 61 ILNGQSFLLTKGSKLNDRAISRSLMDQGNPFLIITKNLKIENSDPYICVEDQKEEVOU 120
DB 61 ILNGQSFLLTKGSKLNDRAISRSLMDQGNPFLIITKNLKIENSDPYICVEDQKEEVOU 120
QY 121 LVFGLTANSDTHLLQGQSLTLTLBSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGQSLTLTLBSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180

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DB 121 LVFGLTANSDTHLLQGQSLTLTLBSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCVTLOKQKVEFKIDIV 200
DB 181 TWTCVTLOKQKVEFKIDIV 200
RESULT 27
AAP94757
ID AAP94757 standard; protein; 402 AA.
XX
AC AAP94757;
XX
DT 25-MAR-2003 (revised)
DT 03-OCT-2002 (revised)
DT 28-JAN-1991 (first entry)
XX
DE Sequence of a secreted form of the CD4 adhesion.
XX
KM HIV; antiviral; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..25 /note="signal"
FT Protein 26..402
XX
PN W08902922-A.
XX
PD 06-APR-1989.
XX
PF 03-OCT-1988; 88WO-US003414.
XX
PR 02-OCT-1987; 87US-00104329.
PR 28-SEP-1988; 88US-00250785.
XX
PA (GENTH ) GENENTECH INC.
XX
PI Capon DJ, Gregory TJ;
XX
DR WPI; 1989-114397/15.
DR N-PSDB; AAN90734.
XX
PT New nucleic acid sequences encoding adhesion. esp. CD 4, variants -
PT partic. with trans-membrane domain inactivated or fused to other peptide,
PT useful esp. for treating HIV infections.
XX
PS Disclosure; Fig 1a-1c; 78pp; English.
XX
CC The patent claims a nucleic acid encoding an aa sequence variant of an
CC adhesion, which is pref. a CD4 polypeptide variant modified such that its
CC transmembrane domain has been inactivated, either deleted or replaced by
CC a sequence of hydrophilic hydrophathy profile. The aa sequence variant of
CC an adhesion may also be a fusion of CD4 with a 2nd polypeptide esp. one
CC contg. a non-CD4 epitope; a signal sequence; a cpd. able to elicit a
CC humoral immune response (viral polypeptide or allergen); or a human
CC plasma protein of long plasma half-life. CD4 fusion proteins can have
CC antiviral and immunomodulatory activity and are esp. useful for treating
CC HIV infections regardless of genetic variation within the virus. They and
CC antibodies raised against them can also be used diagnostically for
CC assaying adhesions and their ligands. (Updated on 03-OCT-2002 to add
CC missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 402 AA;
XX
Query Match 78.1%; Score 1029; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.6e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIQPHKNSNOIK 60
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIQPHKNSNOIK 60

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Db      1 MNRGVPRHLLVLTQLALPAAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNSNOIK 60
QY      61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDTYICEVEDQKEEVOL 120
Db      61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDTYICEVEDQKEEVOL 120
QY      121 LVFGLTANSDPTHLLOQGSFLTLESPPGSSPSVQCRRSPRGKNIQGGKTLSSVQLLEQDSG 180
Db      121 LVFGLTANSDPTHLLOQGSFLTLESPPGSSPSVQCRRSPRGKNIQGGKTLSSVQLLEQDSG 180
QY      181 TWTCTVLQONOKKVEFKIDIV 200
Db      181 TWTCTVLQONOKKVEFKIDIV 200

RESULT 28
AAP91990 ID AAP91990 standard; protein; 458 AA.
XX AC AAP91990;
XX DT 25-MAR-2003 (revised)
DT 15-OCT-1990 (first entry)
XX DE Clone pT4B encoded HIV T4 glycoprotein.
XX KM Human Immunodeficiency Virus T4 envelope glycoprotein; AIDS; ss.
XX OS Synthetic.
XX FH Key
FH FT Peptide 1. .23
FT FT Region /label= leader peptide
FT FT Region /label= variable-like region 1
FT FT Region /label= joining-like region 1
FT FT Region /label= joining-like region 1
FT FT Region /label= variable-like region 2
FT FT Region /label= joining-like region 2
FT FT Region /label= variable-like region 3
FT FT Region /label= joining-like region 3
FT FT Modified-site 297. .299
FT FT Region /label= putative N-glycosylation site
FT FT Region /label= variable-like region 4
FT FT Modified-site 325. .327
FT FT Region /label= putative N-glycosylation site
FT FT Region /label= joining-like region 4
FT FT Region /label= joining-like region 4
FT FT Region /label= trans-membrane region
FT FT Region 421. .458
FT FT /label= cytoplasmic region
XX PN WC0801304-A.
XX PD 25-FEB-1988.
XX PF 20-AUG-1987; 87MO-US002050.
XX PR 21-AUG-1986; 86US-00898587.
XX PA (UYCO-) COLUMBIA UNIV.
XX PA (MADD/) MADDON P J.
XX PI Litman DR, Maddon PJ, Chess L, Axel R, Weiss R, McDougall JS;
XX WPI; 1988-064019/09.
XX DR N-PSDB; AAN80512.

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XX XX
PT Nucleic acid encoding T4 glyco:protein - used for treatment of AIDS and
PT producing antibodies for use as vaccine for immunisation against AIDS.
XX PS Disclosure; Page 7; 128pp; English.
XX CC T4 protein encoded by part of 3kb insert from human T cell library
CC (pT4B). (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 458 AA;
QY Query Match 78.1%; Score 1029; DB 1; Length 458;
Db Best Local Similarity 100.0%; Pred. No. 1,8e-63;
QY 1 MNRGVPRHLLVLTQLALPAAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNSNOIK 60
Db 1 MNRGVPRHLLVLTQLALPAAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNSNOIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDTYICEVEDQKEEVOL 120
Db 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDPTHLLOQGSFLTLESPPGSSPSVQCRRSPRGKNIQGGKTLSSVQLLEQDSG 180
Db 121 LVFGLTANSDPTHLLOQGSFLTLESPPGSSPSVQCRRSPRGKNIQGGKTLSSVQLLEQDSG 180
QY 181 TWTCTVLQONOKKVEFKIDIV 200
Db 181 TWTCTVLQONOKKVEFKIDIV 200

RESULT 29
AAP91369 ID AAP91369 standard; protein; 458 AA.
XX AC AAP91369;
XX DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 08-JAN-1990 (first entry)
XX DE T4 protein.
XX KM T4 protein; human immunodeficiency virus; AIDS; clone pT4B.
XX OS Homo sapiens; (human).
XX FH Key
FH FT Domain 1. .23
FH FT Region 24. .117
FH FT Region 41
FH FT Region 109
FH FT Region 118. .134
FH FT Domain 135. .189
FH FT Region 155
FH FT Region 184
FH FT Domain 190. .204
FH FT Domain 205. .286
FH FT Domain 287. .309
FH FT Binding-site 296. .298
FH FT Domain 310. .376
FH FT Binding-site 325. .327
FH FT Region 328
FH FT Region 370
FH FT Region 377. .397
FH FT Domain 398. .420
FH FT Domain 421. .458
XX PN EPJ30227-A.
XX PD 30-AUG-1989.
XX

```







## RESULT 33

AAR27277 standard; protein; 462 AA.

ID AAR27277 standard; protein; 462 AA.  
XX  
AC AAR27277;  
XX  
DT 25-MAR-2003 (revised)  
DT 28-JUL-1995 (first entry)  
XX  
DE CD4:eta peptide chimeric protein.  
XX  
KW Fusion protein; CD4; extracellular domain; zeta; eta; gamma;  
KW membrane spanning domain; intracellular domain; type I;  
KW integral membrane homodimer; TCR; T cell antigen receptor;  
KW extracellular domain; mouse; human; receptor; chimera;  
KW HBB-ALU tumour cell line; natural killer cell.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Protein 1..399 /note="CD4 extracellular domain"  
FT Protein 400..462 /note="Zeta membrane spanning and intracellular domain"  
FT Protein /note="Zeta membrane spanning and intracellular domain"  
XX  
PN WO9215322-A1.  
XX  
PD 17-SEP-1992.  
XX  
PF 06-MAR-1992; 92MO-US001785.  
XX  
PR 07-MAR-1991; 91US-00665961.  
XX  
PA (GENO) GEN HOSPITAL CORP.  
XX  
PI Seed B, Romeo C, Kolanus W;  
XX  
DR WPI; 1992-331474/40.  
DR N-PSDB; AAQ28705.  
XX  
PT Therapeutic cells expressing chimeric receptors - directing cellular  
PT response to an infective agent, useful in treating HIV-1, AIDS  
XX  
PT Pneumocystis carinii infections etc.  
XX  
PS Example 2; Page 73-74; 114pp; English.  
XX  
XX This sequence represents a fusion protein between the CD4 extracellular  
XX domain and the eta protein membrane spanning domain and intracellular  
XX domain. Eta is an isoform of zeta (see also AAR27276) which is a 32 kD  
XX type I integral membrane homodimer, which arises by alternate mRNA  
XX splicing. It is present in reduced amounts in cells expressing the T cell  
XX antigen receptor. Zeta-eta heterodimers are thought to mediate the  
XX formation of inositol phosphates, as well as the receptor initiated cell  
XX death called apoptosis, in the production of the CD4 receptor chimera,  
XX the eta cDNA was isolated from the HBB-ALU tumour cell line and from  
XX human natural killer cells. The eta cDNA was joined to the extracellular  
XX domain of an engineered form of CD4 possessing a BamHI site just upstream  
XX of the membrane spanning domain, by a BamHI site naturally present a few  
XX residues upstream of the membrane spanning domain. (Updated on 25-MAR-  
XX 2003 to correct PN field.)  
XX  
SQ Sequence 462 AA;

Query Match 78.1%; Score 1029; DB 2; Length 462;  
Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKKGDTVELCTASOKKSIOFHKNSNOIK 60  
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKKGDTVELCTASOKKSIOFHKNSNOIK 60  
QY 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVL 120

DB 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVL 120

QY 121 LVFGLTANSDBTHLLOGOSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVQLBLQDSG 180  
DB 121 LVFGLTANSDBTHLLOGOSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVQLBLQDSG 180

QY 181 TWTCTVLQONQKVEFKIDIV 200  
DB 181 TWTCTVLQONQKVEFKIDIV 200

## RESULT 34

AAR78677 standard; protein; 462 AA.

ID AAR78677 standard; protein; 462 AA.  
XX  
AC AAR78677;  
XX  
DT 16-APR-1996 (first entry)  
XX  
DE T-cell receptor gamma.  
XX  
KW Chimeric receptor; CD4; T-cell receptor gamma; HIV; cytolysis;  
KW human immunodeficiency virus; adoptive immunotherapy.  
XX  
OS Homo sapiens.  
XX  
PN WO9521528-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 12-JAN-1995; 95WO-US000454.  
XX  
PR 14-FEB-1994; 94US-00195395.  
PR 02-AUG-1994; 94US-00284391.  
XX  
PA (GENO) GEN HOSPITAL CORP.  
XX  
PI Seed B, Banapour B, Romeo C, Kolanus W;  
XX  
DR WPI; 1995-292893/38.  
DR P-PSDB; AAQ96123.  
XX  
XX Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing  
XX cells.  
XX  
PS Example 2; Page 77-78; 118pp; English.  
XX  
XX Fusion proteins comprising the extracellular domain of CD4 fused to T-  
XX cell receptor zeta, gamma or eta (AAR78676-78, respectively) were  
XX expressed in CV1 using a vaccine virus vector. These CD4:zeta, CD4:gamma  
XX and CD4:eta chimeric receptors mediated cytolysis of targets expressing  
XX HIV gp120/41  
XX  
SQ Sequence 462 AA;

Query Match 78.1%; Score 1029; DB 2; Length 462;  
Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKKGDTVELCTASOKKSIOFHKNSNOIK 60  
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKKGDTVELCTASOKKSIOFHKNSNOIK 60  
QY 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVL 120  
DB 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVL 120  
QY 121 LVFGLTANSDBTHLLOGOSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVQLBLQDSG 180  
DB 121 LVFGLTANSDBTHLLOGOSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVQLBLQDSG 180  
QY 181 TWTCTVLQONQKVEFKIDIV 200

```

Db      181 TWCTVQLQNKVPEFKIDIV 200
|||||
RESULT 35
AAR89457
ID AAR89457 standard; protein; 462 AA.
XX
AC AAR89457;
XX
DT 26-SEP-1996 (first entry)
XX
DE CD4:gamma fusion protein.
XX
KW CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1;
KM human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
KM dendritic cell; therapy; mammal; infection.
XX
OS Synthetic.
XX
PN W09603883-A1.
XX
PD 15-FEB-1996.
XX
PF 26-JUL-1995; 95WO-US009468.
XX
PR 02-AUG-1994; 94US-00284391.
XX
PR 24-FEB-1995; 95US-00394388.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI Seed B, Banapour B, Romeo C, Kolanus W;
XX
DR WPI; 1996-129034/13.
XX
DR N-PSDB; AAT10802.
XX
PT Membrane-bound chimeric receptor comprising extracellular portion
PT including CD4 fragment - cells expressing receptor can be used for
PT treatment of HIV infection.
XX
XX
PS Example 2; Page 79; 134pp; English.
XX
CC AAT10801-T10803 represent membrane bound proteinaceous chimeric receptors
CC of the invention. This sequence represents the CD4:gamma chimera. The
CC transmembrane region of the chimeric receptor acts to separate the
CC intracellular and extracellular domains of the chimera, and contains a
CC portion of the CD7 (see AAR89440), CD5 or CD34 transmembrane domains.
CC Alternatively, the extracellular portion of the receptor can be separated
CC from the intracellular domain by the hinge, CH2 and CH3 domains of human
CC IgG1 (see AAR89441). The extracellular portion of the chimeric receptor
CC contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4
CC sequence, see AAR89450 and AAR89451) which specifically recognizes and
CC binds HIV-infected cells, but does not mediate HIV infection. The
CC extracellular domain of the receptor is separated from the cell membrane
CC by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The
CC cells expressing the receptor are preferably T cells, B cells,
CC neutrophils, or dendritic cells. The therapeutic cells expressing the
CC chimeric receptor are administered to a mammal to treat HIV infection
XX
SO Sequence 462 AA:
Query Match 78.1%; Score 1029; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.9e-53;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      121 LVFGLTRANSDTHLLQGSLLTLTLESPGSSPSVQCSPRGKNIQGGKTLVSQLEFDQSG 180
|||
Db      121 LVFGLTRANSDTHLLQGSLLTLTLESPGSSPSVQCSPRGKNIQGGKTLVSQLEFDQSG 180
QY      181 TWCTVQLQNKVPEFKIDIV 200
|||||
Db      181 TWCTVQLQNKVPEFKIDIV 200
|||||
RESULT 36
AAW02214
ID AAW02214 standard; protein; 462 AA.
XX
AC AAW02214;
XX
DT 11-NOV-1996 (first entry)
XX
DE CD4:Fc receptor gamma chain chimeric receptor.
XX
KW Chimeric receptor; cellular immunity; adoptive immunotherapy; CD4;
KM human immunodeficiency virus type 1; HIV-1; AIDS; therapy;
KM Fc receptor gamma chain; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Domain 1..393
FT /label= "Extracellular_domain"
FT /note= "CD4 extracellular domain"
FT 394..397
FT /label= "Linker"
FT /note= "encoding DNA contains a BamHI site used for
FT fusion construction"
FT Region 398..462
FT /note= "region of fusion derived from gamma chain,
FT preferred signal-transducing portions for constructs of
FT the invention are amino acids 421-462 and 402-419"
FT 400..462
FT /label= "Transmembrane+intracellular_domains"
XX
PN W09625953-A1.
XX
PD 29-AUG-1996.
XX
PF 25-JAN-1996; 96WO-US001056.
XX
PR 24-FEB-1995; 95US-00394176.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI Seed B, Romeo C, Kolanus W;
XX
DR WPI; 1996-402134/40.
XX
DR N-PSDB; AAT36759.
XX
PT Direction of cellular immune response using therapeutic cell expressing 2
PT chimeric receptors - comprising region binding to target cell and region
PT that signals target cell destruction, or CD28 region, partic. for
PT eliminating HIV-infected cells.
XX
PS Claim 7; Page 76; 120pp; English.
XX
XX
CC A chimeric receptor (AAW02214) comprises the extracellular domain of an
CC engineered form of the CD4 cellular receptor for HIV and the
CC transmembrane and intracellular regions, including the cytoytic signal-
CC transducing portion, of the human Fc receptor gamma chain; the region of
CC the fusion is shown in AAW02223. It can be obtd. by inserting a gene
CC fusion (AAT36759) into a vaccinia virus vector and expression in host
CC cells. Chimeric receptors comprising CD4 fused to Fc receptor gamma or T
CC -cell receptor zeta (see also AAW02213) or eta (AAW02215) chains are
CC capable of directing cytotoxic T lymphocytes to specifically recognise
CC and kill cells expressing HIV gp120, thus providing a therapy for AIDS
XX

```

SQ Sequence 462 AA;  
 Query Match 78.1%; Score 1029; DB 2; Length 462;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTALLPATQGNKVVLGKKDPTVELTCTASQKSIQFMKNSNOIK 60  
 DB 1 MNRGVPRHLLVLTALLPATQGNKVVLGKKDPTVELTCTASQKSIQFMKNSNOIK 60  
 QY 61 ILGNQGSFLTGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEYQL 120  
 DB 61 ILGNQGSFLTGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEYQL 120  
 QY 121 LVFGLTANSPTHTLLGGSLTTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGLTANSPTHTLLGGSLTTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 QY 181 TWCTVQLNQKKEVEFKIDIV 200  
 DB 181 TWCTVQLNQKKEVEFKIDIV 200

RESULT 37  
 AAM83142  
 ID AAM83142 standard; protein; 462 AA.  
 AC AAM83142;  
 DT 03-FEB-1999 (first entry)  
 DE Chimeric receptor containing mouse gamma polypeptide.  
 XX Human; zeta; eta; gamma; membrane-bound chimeric receptor; infection;  
 KM tumour; cancer cell; autoimmune-generated cell; T cell receptor; CD3;  
 KM CD4; B cell receptor; Fc receptor; pathogen; bacterial; fungal;  
 KM protozoan; viral.  
 OS Synthetic.  
 XX Mus sp.  
 PN US5843728-A.  
 PD 01-DEC-1998.  
 XX 05-APR-1995; 95US-00417495.  
 PF 07-MAR-1991; 91US-00665961.  
 PR 06-MAR-1992; 92US-00847566.  
 PR 28-FEB-1994; 94US-00203866.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA Romeo C, Kolanus W, Seed B;  
 PI WPI; 1999-044582/04.  
 DR N-PSDB; AAV70158.  
 XX Membrane-bound chimeric receptors - comprising extracellular portion  
 PT which recognises and binds a target cell and an intracellular portion of  
 PT e.g. a T-cell receptor.  
 XX Example 2; Col 43-46; 57pp; English.

CC or autoimmune-generated cells  
 XX SQ Sequence 462 AA;  
 Query Match 78.1%; Score 1029; DB 2; Length 462;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;  
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTALLPATQGNKVVLGKKDPTVELTCTASQKSIQFMKNSNOIK 60  
 DB 1 MNRGVPRHLLVLTALLPATQGNKVVLGKKDPTVELTCTASQKSIQFMKNSNOIK 60  
 QY 61 ILGNQGSFLTGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEYQL 120  
 DB 61 ILGNQGSFLTGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEYQL 120  
 QY 121 LVFGLTANSPTHTLLGGSLTTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGLTANSPTHTLLGGSLTTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 QY 181 TWCTVQLNQKKEVEFKIDIV 200  
 DB 181 TWCTVQLNQKKEVEFKIDIV 200

RESULT 38  
 AAR27278  
 ID AAR27278 standard; protein; 532 AA.  
 AC AAR27278;  
 DT 25-MAR-2003 (revised)  
 DT 28-JUL-1995 (first entry)  
 DE CD4; gamma peptide chimeric protein.  
 XX Fusion protein; CD4; extracellular domain; zeta; eta; gamma;  
 KM membrane spanning domain; intracellular domain; type I;  
 KM integral membrane homodimer; TCR; T cell antigen receptor;  
 KM extracellular domain; mouse; human; receptor; chimera;  
 KM HPB-ALL tumour cell line; natural killer cell.  
 OS Homo sapiens.  
 PN WO9215322-A1.  
 PD 17-SEP-1992.  
 PF 06-MAR-1992; 92WO-US001785.  
 PR 07-MAR-1991; 91US-00665961.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA Seed B, Romeo C, Kolanus W;  
 PI WPI; 1992-331474/40.  
 DR N-PSDB; AAQ28706.  
 XX Therapeutic cells expressing chimeric receptors - directing cellular  
 PT response to an infective agent, useful in treating HIV-1, AIDS  
 PT Pneumocystis carinii infections etc.  
 XX Example 2; Page 74-76; 114pp; English.

This sequence represents a fusion protein between the CD4 extracellular  
 domain and the gamma protein membrane spanning domain and intracellular  
 domain. The Fc-receptor-associated gamma chain is expressed in cell  
 surface complexes with additional polypeptides, some of which mediate  
 ligand recognition, and others which have undefined function. Gamma bears  
 a homodimeric structure and overall organisation very similar to that of  
 zeta (see also AAQ28704), and is a component of both the mast  
 cell/basophil high affinity IgE receptor, Fc-epsilon-RI, which consists

of at least three distinct polypeptide chains and one of the low affinity receptor for IgG, represented in mice by Fc-gamma-R1-alpha. In the production of the CD4 receptor chimera, the gamma cDNA was isolated from the HBB-MuL tumour cell line and from human natural killer cells. The gamma cDNA was joined to the extracellular domain by engineering a BamHI site just upstream of the membrane spanning domain, by a BamHI site naturally present a few residues upstream of the membrane spanning domain. (updated on 25-MAR-2003 to correct FN field.)

CC XX Sequence 532 AA;

Query Match 78.1%; Score 1029; DB 2; Length 532;  
Best Local Similarity 100.0%; Pred. No. 2, 2e-63;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALLPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60  
DB 1 MNRGVPFRHLILVQLALLPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60  
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKIKIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKIKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSPTHLIQGQSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSPTHLIQGQSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWICTVLQONOKKVEFKIDIV 200  
DB 181 TWICTVLQONOKKVEFKIDIV 200

RESULT 39

AA878678 ID AAR78678 standard; protein; 532 AA.

AC AAR78678;

DT 16-APR-1996 (first entry)

DE T-cell receptor eta.

KM Chimeric receptor; CD4; T-cell receptor eta; HIV; cytolysis;  
KW human immunodeficiency virus; adoptive immunotherapy.

OS Homo sapiens.

PN MO9521528-A1.

PD 17-AUG-1995.

PF 12-JAN-1995; 95W0-US000454.

PR 14-FEB-1994; 94US-00195395.

PR 02-AUG-1994; 94US-00284391.

PA (GEHO) GEN HOSPITAL CORP.

PI Seed B, Banapour B, Romeo C, Kolanus W;

DR WPI; 1995-292893/38.

DR N-PSDB; AAQ96124.

PT Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing cells.

PS Example 2; Page 78-79; 118pp; English.

CC Fusion proteins comprising the extracellular domain of CD4 fused to T-cell receptor zeta, gamma or eta (AAR78676-78, respectively) were expressed in CV1 using a vaccine virus vector. These CD4:zeta, CD4:gamma and CD4:eta chimeric receptors mediated cytolysis of targets expressing HIV gp120/41

XX Sequence 532 AA;

Query Match 78.1%; Score 1029; DB 2; Length 532;  
Best Local Similarity 100.0%; Pred. No. 2, 2e-63;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALLPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60  
DB 1 MNRGVPFRHLILVQLALLPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60  
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKIKIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKIKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSPTHLIQGQSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSPTHLIQGQSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWICTVLQONOKKVEFKIDIV 200  
DB 181 TWICTVLQONOKKVEFKIDIV 200

RESULT 40

AA89458 ID AAR89458 standard; protein; 532 AA.

AC AAR89458;

DT 26-SEP-1996 (first entry)

DE CD4:eta fusion protein.

KM CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1;  
KW human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;  
KW dendritic cell; therapy; mammal; infection.

OS Synthetic.

PN MO9603883-A1.

PD 15-FEB-1996.

PF 26-JUL-1995; 95W0-US009468.

PR 02-AUG-1994; 94US-00284391.

PR 24-FEB-1995; 95US-00394388.

PA (GEHO) GEN HOSPITAL CORP.

PI Seed B, Banapour B, Romeo C, Kolanus W;

DR WPI; 1996-129034/13.

DR N-PSDB; AAT10803.

PT Membrane-bound chimeric receptor comprising extracellular portion including CD4 fragment - cells expressing receptor can be used for treatment of HIV infection.

PS Example 2; Page 80-81; 134pp; English.

CC AAT10801-T10803 represent membrane bound proteinaceous chimeric receptors of the invention. This sequence represents the CD4:eta chimera. The transmembrane region of the chimeric receptor acts to separate the intracellular and extracellular domains of the chimera, and contains a portion of the CD7 (see AAR89440), CD5 or CD34 transmembrane domains. Alternatively, the extracellular portion of the receptor can be separated from the intracellular domain by the hinge, CH2 and CH3 domains of human IgG1 (see AAR89441). The extracellular portion of the chimeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence, see AAR89450 and AAR89451) which specifically recognises and binds HIV-infected cells, but does not mediate HIV infection. The

CC extracellular domain of the receptor is separated from the cell membrane  
CC by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The  
CC cells expressing the receptor are preferably T cells, B cells,  
CC neutrophils, or dendritic cells. The therapeutic cells expressing the  
CC chimeric receptor are administered to a mammal to treat HIV infection  
XX  
SQ Sequence 532 AA;

Query Match 78.1%; Score 1029; DB 2; Length 532;  
Best Local Similarity 100.0%; Pred. No. 2.2e-63;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLTQALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHWKNSNQIK 60  
DB 1 MNRGVPFRHLVLTQALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHWKNSNQIK 60  
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEEYQL 120  
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEEYQL 120  
QY 121 LVFGLTANSPTHTLLOGQSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSPTHTLLOGQSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCTVLQONOKKVEFKIDIV 200  
DB 181 TWTCTVLQONOKKVEFKIDIV 200

RESULT 41  
AAW02215  
ID AAW02215 standard; protein; 532 AA.

XX AAW02215;  
AC AAW02215;  
XX 16-OCT-2003 (revised)  
DT 11-NOV-1996 (first entry)  
DE CD4:T-cell receptor eta chain chimeric receptor.  
XX  
XX Chimeric receptor; cellular immunity; adoptive immunotherapy; CD4;  
KM human immunodeficiency virus type 1; HIV-1; AIDS; therapy;  
KM T-cell receptor eta chain; cytotoxic T lymphocyte; CTL.  
XX  
XX Homo; sapiens.  
OS Mus sp.  
OS Chimeric.  
OS  
FH Key  
FT Domain  
FT Location/Qualifiers  
FT /label= "Extracellular domain"  
FT /note= "CD4 extracellular domain"  
FT 394..396  
FT /label= linker  
FT /note= "encoding DNA contains a BamHI site used for  
FT fusion construction"  
FT 397..532  
FT /note= "region of fusion derived from eta chain,  
FT preferred signal-transducing portions for constructs of  
FT the invention are amino acids 421-532, 423-455, 438-455,  
FT 461-494, 494-528 or 400-420"  
FT 400..437  
FT /label= "Transmembrane domain"  
FT /note= "eta chain transmembrane domain"  
FT 438..575  
FT /label= "Intracellular domain"  
FT /note= "eta chain intracellular domain"

XX WO9625953-A1.  
XX 29-AUG-1996.  
XX 25-JAN-1996; 96WO-US001056.

XX 24-FEB-1995; 95US-00394176.  
PR (GEHO) GEN HOSPITAL CORP.  
XX  
XX  
XX Seed B, Romeo C, Kolanus W;  
XX  
XX WPI; 1996-402134/40.  
DR N-PSDB; AAT36760.  
XX

PT Direction of cellular immune response using therapeutic cell expressing 2  
PT chimeric receptors - comprising region binding to target cell and region  
PT that signals target cell destruction, or CD28 region, partic. for  
PT eliminating HIV-infected cells.  
XX  
XX

PS Claim 7, Page 77-78; 120pp; English.

XX A chimeric receptor (AAW00215) comprises the extracellular domain of an  
XX engineered form of the CD4 cellular receptor for HIV and the  
XX transmembrane and intracellular regions, including the cytosolic signal-  
XX transducing portion, of the mouse T-cell receptor eta chain. It can be  
XX obtd. by inserting a gene fusion (AAT36760) into a vaccinia virus vector  
XX and expression in host cells. Chimeric receptors comprising CD4 fused to  
XX eta, eta (see also AAW02213) or Fc receptor gamma (see also AAW02214)  
XX chains are capable of directing cytotoxic T lymphocytes to specifically  
XX recognise and kill cells expressing HIV gp120, thus providing a therapy  
XX for AIDS. (Updated on 16-OCT-2003 to standardise OS field)  
XX

SQ Sequence 532 AA;

Query Match 78.1%; Score 1029; DB 2; Length 532;  
Best Local Similarity 100.0%; Pred. No. 2.2e-63;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLTQALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHWKNSNQIK 60  
DB 1 MNRGVPFRHLVLTQALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHWKNSNQIK 60  
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEEYQL 120  
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEEYQL 120  
QY 121 LVFGLTANSPTHTLLOGQSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSPTHTLLOGQSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCTVLQONOKKVEFKIDIV 200  
DB 181 TWTCTVLQONOKKVEFKIDIV 200

RESULT 42  
AAW83141  
ID AAW83141 standard; protein; 532 AA.

XX AAW83141;  
AC AAW83141;  
XX  
XX 03-FEB-1999 (first entry)  
DT  
DE Chimeric receptor containing human eta polypeptide.  
XX  
XX Human; zeta; eta; gamma; membrane-bound chimeric receptor; infection;  
KM tumour; cancer cell; autoimmune-generated cell; T cell receptor; CD3;  
KM CD4; B cell receptor; Fc receptor; pathogen; bacterial; fungal;  
KM protozoan; viral.  
XX  
XX Synthetic.  
OS Homo sapiens.  
OS  
OS  
XX  
XX US5843728-A.  
XX  
XX 01-DEC-1998.

```

PF 05-APR-1995; 95US-00417495.
XX
PR 07-MAR-1991; 91US-00665961.
PR 06-MAR-1992; 92US-00847566.
PR 28-FEB-1994; 94US-00203866.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
PI Romeo C, Kolanus W, Seed B;
XX
DR WPI; 1999-044582/04.
DR N-PSDB; AAV70157.
XX
XX Membrane-bound chimeric receptors - comprising extracellular portion
PT which recognises and binds a target cell and an intracellular portion of
PT e.g. a T-cell receptor.
XX
XX Claim 11; Col 45-48; 57pp; English.
XX
XX The present invention describes DNA encoding a membrane-bound chimeric
CC receptor comprising: (a) an extracellular portion that specifically
CC recognises and binds a target cell or a target infective agent; and (b)
CC an intracellular portion of a T-cell receptor CD3, zeta or eta
CC polypeptide, a B-cell receptor polypeptide or an FC receptor polypeptide.
CC The present sequence represents a chimeric receptor containing the human
CC eta polypeptide. Cells expressing chimeric receptors of the present
CC invention can be administered to mammals in order to destroy pathogens
CC (e.g. bacteria, fungi, protozoa or viruses, especially HIV), cancer cells
CC or autoimmune-generated cells
XX
SQ Sequence 532 AA;

Query Match 78.1%; Score 1029; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 2.2e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKKSIOFHWKNSQIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKKSIOFHWKNSQIK 60

QY 61 ILGNQGSFLTQKSPSKLNDRADSRSLWDOGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTQKSPSKLNDRADSRSLWDOGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120

QY 121 LVFGLTANSDTHLLQGSQSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSQSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180

QY 181 TWTCTVLQONQKVEFKIDIV 200
DB 181 TWTCTVLQONQKVEFKIDIV 200

RESULT 43
AAR27276
ID AAR27276 standard; protein; 575 AA.
XX
AC AAR27276;
XX
DT 25-MAR-2003 (revised)
DT 28-JUL-1995 (first entry)
XX
DE CD4: zeta peptide chimeric protein.
XX
XX Fusion protein; CD4; extracellular domain; zeta; eta; gamma;
XX membrane spanning domain; intracellular domain; type I;
XX integral membrane homodimer; TCR; T cell antigen receptor;
XX extracellular domain; mouse; human; receptor; chimera;
XX HBB-ALL tumour cell line; natural killer cell.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

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FT Protein 1..399
FT /note="CD4 extracellular domain"
FT Protein 400..575
FT /note="Zeta membrane spanning and intracellular domain"
XX
XX WO9215322-A1.
XX
XX 17-SEP-1992.
XX
XX 06-MAR-1992; 92MO-US001785.
XX
XX 07-MAR-1991; 91US-00665961.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B, Romeo C, Kolanus W;
XX
XX WPI; 1992-331474/40.
XX
XX N-PSDB; AAQ28704.
XX
XX Therapeutic cells expressing chimeric receptors - directing cellular
PT response to an infective agent, useful in treating HIV-1, AIDS
PT Pneumocystis carinii infections etc.
XX
XX Example 2; Page 72-73; 114pp; English.
XX
XX This sequence represents a fusion protein between the CD4 extracellular
CC domain and the zeta protein membrane spanning domain and intracellular
CC domain. Zeta is a 32 kD type I integral membrane homodimer which has a 9
CC residue extracellular domain and a 112/113 residue intracellular domain
CC for mouse and human protein respectively. In the production of the CD4
CC receptor chimera, the zeta cDNA was isolated from the HBB-ALL tumour cell
CC line and from human natural killer cells. The zeta cDNA was joined to the
CC extracellular domain of an engineered form of CD4 possessing a BamHI site
CC just upstream of the membrane spanning domain, by a BamHI site naturally
CC present a few residues upstream of the membrane spanning domain. (updated
CC on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 575 AA;

Query Match 78.1%; Score 1029; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKKSIOFHWKNSQIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKKSIOFHWKNSQIK 60

QY 61 ILGNQGSFLTQKSPSKLNDRADSRSLWDOGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTQKSPSKLNDRADSRSLWDOGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120

QY 121 LVFGLTANSDTHLLQGSQSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSQSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180

QY 181 TWTCTVLQONQKVEFKIDIV 200
DB 181 TWTCTVLQONQKVEFKIDIV 200

RESULT 44
AAR78676
ID AAR78676 standard; protein; 575 AA.
XX
XX AAR78676;
XX
DT 16-APR-1996 (first entry)
DT T-cell receptor zeta.
XX
XX T-cell receptor zeta.
XX
XX Chimeric receptor; CD4; T-cell receptor zeta; HIV; cytolysis;
XX human immunodeficiency virus; adoptive immunotherapy.

```

```
XX OS Homo sapiens.
XX XX WO9521528-A1.
XX XX
XX PD 17-AUG-1995.
XX PF 12-JAN-1995; 95WO-US000454.
XX PR 14-FEB-1994; 94US-00195395.
XX PR 02-AUG-1994; 94US-00284391.
XX PA (GENO ) GEN HOSPITAL CORP.
XX PI Seed B, Banapour B, Romeo C, Kolanus W;
XX DR WPI; 1995-292893/38.
XX DR N-PSDB; AAQ96122.
XX PT Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing
XX PT cells.
XX PS Example 2; Page 76-77; 118pp; English.
XX CC Fusion proteins comprising the extracellular domain of CD4 fused to T-
XX CC cell receptor zeta, gamma or eta (AAR78676-78, respectively) were
XX CC expressed in CV1 using a vaccine virus vector. These CD4:zeta, CD4:gamma
XX CC and CD4:eta chimeric receptors mediated cytolysis of targets expressing
XX CC HIV gp120/41
XX SQ Sequence 575 AA:
XX
Query Match 78.1%; Score 1029; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MNRGVPFRHLLVLTQALLPAATQGNKVVLGKKGTVELTCTASQKKSIOFHWKNSNQIK 60
DB 1 MNRGVPFRHLLVLTQALLPAATQGNKVVLGKKGTVELTCTASQKKSIOFHWKNSNQIK 60
QY 61 ILNGQGSFLTKGPKSKLNDRADSRSLMDQGNPPLIKNKIKEDSDPYICEVEDQKEEYOL 120
DB 61 ILNGQGSFLTKGPKSKLNDRADSRSLMDQGNPPLIKNKIKEDSDPYICEVEDQKEEYOL 120
QY 121 LVFGLTANSPTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGKTLVSQLELDQSG 180
QY 181 TWTCVTVLQNKQKVEFKIDIV 200
DB 181 TWTCVTVLQNKQKVEFKIDIV 200
XX
RESULT 45
AAR89456
ID AAR89456 standard; protein; 575 AA.
XX
AC AAR89456;
XX
XX 26-SEP-1996 (first entry)
XX
DE CD4:zeta fusion protein.
XX
XX CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1;
XX KM human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
XX KM dendritic cell; therapy; mammal; infection.
XX
XX OS Synthetic.
XX XX
XX XX WO9603883-A1.
XX XX
XX PD 15-FEB-1996.
XX XX
```

```
PF 26-JUL-1995; 95WO-US009468.
XX
XX PR 02-AUG-1994; 94US-00284391.
XX PR 24-FEB-1995; 95US-00394388.
XX XX
XX PA (GENO ) GEN HOSPITAL CORP.
XX PI Seed B, Banapour B, Romeo C, Kolanus W;
XX PI PI WPI; 1996-129034/13.
XX DR N-PSDB; AAT10801.
XX
XX PT Membrane-bound chimeric receptor comprising extracellular portion
XX PT including CD4 fragment - cells expressing receptor can be used for
XX PT treatment of HIV infection.
XX
XX PS Example 2; Page 77-78; 134pp; English.
XX
XX CC AAT10801-710803 represent membrane bound proteinaceous chimeric receptors
XX CC of the invention. This sequence represents the CD4:zeta chimera. The
XX CC transmembrane region of the chimeric receptor acts to separate the
XX CC intracellular and extracellular domains of the chimera, and contains a
XX CC portion of the CD7 (see AAR89440), CD5 or CD34 transmembrane domains.
XX CC Alternatively, the extracellular portion of the receptor can be separated
XX CC from the intracellular domain by the hinge, CH2 and CH3 domains of human
XX CC IgG1 (see AAR89441). The extracellular portion of the chimeric receptor
XX CC contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4
XX CC sequence, see AAR89450 and AAR89451) which specifically recognizes and
XX CC binds HIV-infected cells, but does not mediate HIV infection. The
XX CC extracellular domain of the receptor is separated from the cell membrane
XX CC by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The
XX CC cells expressing the receptor are preferably T cells, B cells,
XX CC neutrophils, or dendritic cells. The therapeutic cells expressing the
XX CC chimeric receptor are administered to a mammal to treat HIV infection
XX
XX SQ Sequence 575 AA:
XX
Query Match 78.1%; Score 1029; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MNRGVPFRHLLVLTQALLPAATQGNKVVLGKKGTVELTCTASQKKSIOFHWKNSNQIK 60
DB 1 MNRGVPFRHLLVLTQALLPAATQGNKVVLGKKGTVELTCTASQKKSIOFHWKNSNQIK 60
QY 61 ILNGQGSFLTKGPKSKLNDRADSRSLMDQGNPPLIKNKIKEDSDPYICEVEDQKEEYOL 120
DB 61 ILNGQGSFLTKGPKSKLNDRADSRSLMDQGNPPLIKNKIKEDSDPYICEVEDQKEEYOL 120
QY 121 LVFGLTANSPTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGKTLVSQLELDQSG 180
QY 181 TWTCVTVLQNKQKVEFKIDIV 200
DB 181 TWTCVTVLQNKQKVEFKIDIV 200
XX
RESULT 46
AAW02213
ID AAW02213 standard; protein; 575 AA.
XX
AC AAW02213;
XX
XX 11-NOV-1996 (first entry)
XX
DE CD4:T-cell receptor zeta chain chimaeric receptor.
XX
XX KM Chimaeric receptor; cellular immunity; adoptive immunotherapy; CD4;
XX KM human immunodeficiency virus type 1; HIV-1; AIDS; therapy;
XX KM T-cell receptor zeta chain; cytotoxic T lymphocyte; CTL.
XX
XX OS Homo sapiens.
```



```

XX Key Location/Qualifiers
FH 1. .393
FT Domain /label= "Extracellular domain"
FT /note= "CD4 extracellular domain"
FT Region 394. .396
FT /label= Linker
FT /note= "encoding DNA contains a BamHI site used for
FT fusion construction"
FT Region 397. .575
FT /note= "region of fusion derived from zeta chain,
FT preferred signal-transducing portions for constructs of
FT the invention are amino acids 421-575, 423-255, 438-455,
FT 461-494, 494-528, 400-420 and 421-462"
FT Domain 400. .437
FT /label= Transmembrane_domain
FT /note= "zeta chain transmembrane domain"
FT Domain 438. .575
FT /label= Intracellular domain
FT /note= "zeta chain intracellular domain"
XX
XX MO625953-A1.
XX
XX 29-AUG-1996.
XX
XX 25-JAN-1996; 96WO-US001056.
XX
XX 24-FEB-1995; 95US-00394176.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B, Romeo C, Kolanus W;
XX
XX WPI: 1996-402134/40.
XX
XX N-PSDB; AAT36758.
XX
XX Direction of cellular immune response using therapeutic cell expressing 2
XX chimeric receptors - comprising region binding to target cell and region
XX that signals target cell destruction, or CD28 region, partic. for
XX eliminating HIV-infected cells.
XX
XX Claim 7; Page 74-75; 120pp; English.
XX
XX A chimeric receptor (AAW02213) comprises the extracellular domain of an
XX engineered form of the CD4 cellular receptor for HIV and the
XX transmembrane and intracellular regions, including the cytosolic signal-
XX transducing portion, of the human T-cell receptor zeta chain; the region
XX of the fusion is shown in AAW02221. It can be obtd. by inserting a gene
XX fusion (AAT36758) into a vaccinia virus vector and expression in host
XX cells. Chimeric receptors comprising CD4 fused to zeta, eta (see also
XX AAW02215) or Fc receptor gamma (see also AAW02214) chains are capable of
XX directing cytotoxic T lymphocytes to specifically recognise and kill
XX cells expressing HIV gp120, thus providing a therapy for AIDS
XX
XX Sequence 575 AA;
XX
Query Match 78.1%; Score 1029; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 2,4e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 181 TWTCTVLQNGKKEFKIDIV 200
|||||
RESULT 47
AAW83140
ID AAW83140 standard; protein; 575 AA.
XX
XX AAW83140;
XX
XX 03-FEB-1999 (first entry)
XX
XX Chimeric receptor containing human zeta polypeptide.
XX
XX Human; zeta; eta; gamma; membrane-bound chimeric receptor; infection;
XX tumour; cancer cell; autoimmune-generated cell; T cell receptor; CD3;
XX CD4; B cell receptor; Fc receptor; pathogen; bacterial; fungal;
XX protozoan; viral.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX US5843728-A.
XX
XX 01-DEC-1998.
XX
XX 05-APR-1995; 95US-00417495.
XX
XX 07-MAR-1991; 91US-00665961.
XX
XX 06-MAR-1992; 92US-00847566.
XX
XX 28-FEB-1994; 94US-00203866.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Romeo C, Kolanus W, Seed B;
XX
XX WPI: 1999-044582/04.
XX
XX N-PSDB; AAW70156.
XX
XX Membrane-bound chimeric receptors - comprising extracellular portion
XX of which recognises and binds a target cell and an intracellular portion of
XX e.g. a T-cell receptor.
XX
XX Example 2; Col 39-42; 57pp; English.
XX
XX The present invention describes DNA encoding a membrane-bound chimeric
XX receptor comprising: (a) an extracellular portion that specifically
XX recognises and binds a target cell or a target infective agent; and (b)
XX an intracellular portion of a T-cell receptor CD3, zeta or eta
XX polypeptide, a B-cell receptor polypeptide or an Fc receptor polypeptide.
XX The present sequence represents a chimeric receptor containing the human
XX zeta polypeptide. Cells expressing chimeric receptors of the present
XX invention can be administered to mammals in order to destroy pathogens
XX (e.g. bacteria, fungi, protozoa or viruses, especially HIV), cancer cells
XX or autoimmune-generated cells
XX
XX Sequence 575 AA;
XX
Query Match 78.1%; Score 1029; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 2,4e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 181 TWCTVLOKQKVEFKIDIV 200  
 |||||  
 DB 181 TWCTVLOKQKVEFKIDIV 200

## RESULT 48

AA04032  
 ID AAR04032 standard; protein; 2037 AA.  
 XX AAR04032;

AC 25-MAR-2003 (revised)  
 DT 31-OCT-2002 (revised)  
 DT 29-MAY-1990 (first entry)

DE Full length T4 encoded by plasmid PBG381.

KW Soluble T4; PBG381; anti-retroviral agent; AIDS; ARC; HIV; AZT.

OS Synthetic.

PN WO8911860-A.

PD 14-DEC-1989.

PF 08-JUN-1989; 89MO-US002453.

PR 10-JUN-1988; 88US-00204645.

PR 20-APR-1989; 89US-00341080.

PA (BIOJ ) BIOGEN NV INC.

PA (GEHO ) GEN HOSPITAL CORP.

PA (BIOJ ) BIOGEN INC.

PI (BIOJ ) BIOGEN INC.

PI Fisher RA, Schooley RT, Hirsch MS, Johnson VA, Walker BD;

DR WPI; 1990-007302/01.

DR N-PSDB; AAQ03006.

PT Combinations of soluble T4 protein and anti-retro-viral agent - having

PT synergistic activity in treatment and prevention of AIDS, arc and HIV

PT infection.

PS Disclosure; Fig 2; 100bp; English.

CC X = stop codon. The sequence was deduced from the cDNA insert of PBG183.

CC Soluble T4 constructs may be produced by truncating this sequence to give

CC fragments from position 400 to 799, removing the transmembrane and

CC intracytoplasmic domains whilst retaining the extracellular region

CC responsible for HIV binding. The sol. T4 is combined with an anti-viral

CC agent such as AZT. See also AAQ03005. (Updated on 31-OCT-2002 to add

CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 2037 AA;

QY 1 MNRGVPFRHLILVQLALIPATQGNKVVLGKKGDTVELTCTASOKKSIQFHKNSNQIK 60  
 |||||  
 DB 403 MNRGVPFRHLILVQLALIPATQGNKVVLGKKGDTVELTCTASOKKSIQFHKNSNQIK 462  
 |||||  
 QY 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
 |||||  
 DB 463 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 522  
 |||||  
 QY 121 LVFGILTANSDTHLLOGOSLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
 |||||  
 DB 523 LVFGILTANSDTHLLOGOSLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELQDSG 582  
 |||||

QY 181 TWCTVLOKQKVEFKIDIV 200  
 |||||  
 DB 583 TWCTVLOKQKVEFKIDIV 602

## RESULT 49

AA07641  
 ID AAR07641 standard; protein; 2050 AA.  
 XX AAR07641;

AC 31-OCT-2002 (revised)

DT 20-DEC-1990 (first entry)

DE Deduced sequence of PBG381 comprising truncated T4 glycoprotein.

KW plasmid PBG381; soluble T4 protein; AIDS; ARC; HIV.

OS Synthetic.

PN WO9008198-A.

PD 26-JUL-1990.

PF 18-JAN-1989; 89US-00300096.

PR 18-JAN-1989; 89US-00300096.

PR 18-JAN-1989; 89US-00300096.

PA (HARD ) HARVARD COLLEGE.

PI Letvin NA;

DR WPI; 1990-254040/33.

DR N-PSDB; AAQ05608.

PT Treating or preventing AIDS, ARC or HIV infection - by administering an

PT immunologically effective amt. of soluble T4 protein.

PS Disclosure; Fig 2; 121bp; English.

CC Entire sequence translation of plasmid PBG381 used to transform Chinese

CC Hamster Ovary cells for the production of soluble truncated T4.

CC Transmembrane and cytoplasmic domain-encoding regions are deleted from

CC the T4 CDS to encode a truncated protein. The soluble forms may be

CC modified to increase their immunogenicity by addition of an adjuvant such

CC as incomplete Freund's adjuvant. The T4 interferes with HIV/T4

CC interaction and elicits anti-soluble T4 antibody prodn. See also

CC AAQ05607. (Updated on 31-OCT-2002 to add missing OS field.)

XX Sequence 2050 AA;

QY 1 MNRGVPFRHLILVQLALIPATQGNKVVLGKKGDTVELTCTASOKKSIQFHKNSNQIK 60  
 |||||

DB 403 MNRGVPFRHLILVQLALIPATQGNKVVLGKKGDTVELTCTASOKKSIQFHKNSNQIK 462  
 |||||

QY 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
 |||||

DB 463 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 522  
 |||||

QY 121 LVFGILTANSDTHLLOGOSLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
 |||||

DB 523 LVFGILTANSDTHLLOGOSLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELQDSG 582  
 |||||

Db 583 TWTCVLONOKVEFKIDIV 602

RESULT 50  
AAR26532  
ID AAR26532 standard; protein; 310 AA.  
XX  
AC AAR26532;  
XX  
DT 25-MAR-2003 (revised)  
DT 28-JAN-1993 (first entry)  
XX  
DE Sequence of CD4-kappa chimeric light chain heterotetramer.  
XX  
KM CD4-gamma 1 chimeric heavy chain homodimer; expression vector; HIV;  
KM therapy; diagnostic agent; inhibition.  
XX  
OS Synthetic.  
XX  
FH Key  
FT Region 1..204  
FT /label= CD4  
FT /note= "1..25 = preregion"  
FT 205..310  
FT /label= C kappa  
XX  
PN WO9213559-A1.  
XX  
XX 20-AUG-1992.  
XX  
PD 10-FEB-1992; 92WO-US001152.  
XX  
PF 08-FEB-1991; 91US-00654205.  
XX  
PR (PROG-) PROGENICS PHARM INC.  
XX  
PA Beaudry GA, Maddon PJ;  
XX  
PI WPI; 1992-299758/36.  
XX  
DR N-PSDB; AA027832.  
XX  
PT CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector -  
PT for preventing and treating HIV infection useful as a diagnostic agent.  
XX  
PS Example; Fig 5; 88pp; English.  
XX  
CC The human kappa light chain constant region is excised from the plasmid  
CC pCkappa light and ligated to M13mp18. The purified vector containing the  
CC kappa light chain constant region is then ligated to human CD4 cDNA. The  
CC cDNA is used to prepare an expression vector encoding the light chains of  
CC a CD4-IgG1 chimeric heterotetramer designated CD4-KLC-prcCMV (ATCC  
CC 75194). (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 310 AA;

Query Match 78.0%; Score 1027; DB 2; Length 310;  
Best Local Similarity 84.8%; Pred. No. 1.6e-63;  
Matches 207; Conservative 4; Mismatches 21; Indels 12; Gaps 1;

QY 1 MNRGVPFRHLILVQLALPAATGKNKVLGKGDVETLCTASQKSIQPHWNSNQIK 60  
DB 1 MNRGVPFRHLILVQLALPAATGKNKVLGKGDVETLCTASQKSIQPHWNSNQIK 60  
QY 61 ILNGQSFLLTKGPKLNDRADSRSLWDQGNFLLIINKLIEDSDTYICEVEDQKEEVQL 120  
DB 61 ILNGQSFLLTKGPKLNDRADSRSLWDQGNFLLIINKLIEDSDTYICEVEDQKEEVQL 120  
QY 121 LVFELTNSDTHLLOSGSLTTLSPGSSPSVOCRSBRGNIOGGLTSLVSQLELDDSG 180  
DB 121 LVFELTNSDTHLLOSGSLTTLSPGSSPSVOCRSBRGNIOGGLTSLVSQLELDDSG 180  
QY 181 TWTCVLONOKVEFKIDIVRASALPAPPTGSLPDPQTASALPDPASALPALAVI 240  
DB 181 TWTCVLONOKVEFKIDIVRASALPAPPTGSLPDPQTASALPDPASALPALAVI 240

Db 181 TWTCVLONOKVEFKIDIVIAFTVAAP-----SVFIPEPSDEQLKSGTASY 228

QY 241 SFLL 244  
DB 229 VCLL 232

RESULT 51  
AAR46679  
ID AAR46679 standard; protein; 530 AA.  
XX  
AC AAR46679;  
XX  
DT 25-MAR-2003 (revised)  
DT 08-AUG-1994 (first entry)  
XX  
DE CD4-IgG2 chimeric heavy chain.  
XX  
KM CD4; gamma; heavy chain; chimeric; chimeric; immunconjugate; HIV;  
KM human immunodeficiency virus; radionuclide; toxin; therapy; treatment;  
KM imaging; detection; targeting; immunoglobulin; IgG.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT Region 1..204  
FT /label= CD4 Region.  
FT 205..302  
FT /label= CH1 Region.  
FT 303..314  
FT /label= Hinge Region.  
FT 315..423  
FT /label= CH2 Region.  
FT 424..530  
FT /label= CH3 Region.  
XX  
PN WO9403191-A1.  
XX  
XX 17-FEB-1994.  
XX  
PD 06-AUG-1993; 93WO-US007422.  
XX  
PF 07-AUG-1992; 92US-00927931.  
XX  
PR (PROG-) PROGENICS PHARM INC.  
XX  
PA Allaway GP, Maddon PJ;  
XX  
PI WPI; 1994-065392/08.  
XX  
DR N-PSDB; AA055751.  
XX  
PT Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2  
PT immunoconjugates - used to kill HIV-infected cells and to image and  
PT stage HIV infection.  
XX  
PS Disclosure; Fig 4; 142pp; English.  
XX  
CC A tetramer comprising 2 IgG2 heavy chains or two CD4-IgG2 chimeric heavy  
CC chains and two kappa light chains or CD4-kappa light chains (AAR46680)  
CC linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide  
CC of low to moderate cytotoxicity. The resulting immunoconjugate comprising  
CC the toxin can be used to kill HIV infected cells and to treat HIV  
CC infected subjects to reduce the population of HIV infected cells. It can  
CC also be used to reduce the likelihood of infection. The immunoconjugate  
CC comprising the radionuclide can be used to image HIV infected tissue, to  
CC calculate the stage of HIV infection or the efficacy of an anti-HIV  
CC treatment using the imaging technique and for determining the prognosis  
CC of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 530 AA;

Query Match 77.9%; Score 1026.5; DB 2; Length 530;  
Best Local Similarity 84.4%; Pred. No. 3.2e-63;

Matches 206; Conservative 6; Mismatches 21; Indels 11; Gaps 1;  
QY 1 MNRGVPFRHLVLTALPAATQGNKVLTGKKGDTVELTCTASOKKSTIOFHKNSNOIK 60  
DB 1 MNRGVPFRHLVLTALPAATQGNKVLTGKKGDTVELTCTASOKKSTIOFHKNSNOIK 60  
QY 61 ILGNQGSFLTKGPSKLTNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEYVL 120  
DB 61 ILGNRGSFLTKGPSKLTNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEYVL 120  
QY 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPSVQCRSPRGKNIQGKTLVSQLEIQDSG 180  
DB 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPSVQCRSPRGKNIQGKTLVSQLEIQDSG 180  
QY 181 TWTCTVLQONOKKVEPKIDIVPRASALPAPTGSALPDPTASALPPPPASALPALAVI 240  
DB 181 TWTCTVLQONOKKVEPKIDIVVLAFASTKGP-----SVFPLAFCSRSTSESTAAI 229  
QY 241 SFLL 244  
DB 230 GCLIV 233  
RESULT 52  
AAP93506  
ID AAP93506 standard; protein; 394 AA.  
XX AAP93506;  
AC 25-MAR-2003 (revised)  
DT 02-JUN-1990 (first entry)  
XX  
XX  
DE Derived sequence of soluble T4 lymphocyte surface protein (sT4).  
KM Soluble T4 lymphocyte surface protein; sT4; AIDS therapy; AIDS diagnosis.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Protein 26..394  
FT Misc-difference 26..26  
FT /note= "When sequence was determined by amino acid  
FT sequencing, this residue was Lys." 27..45  
FT Region /note= "These residues are identical to those determined  
FT by amino acid sequencing"  
XX  
XX EPJ13377-A.  
XX  
XX  
XX 26-APR-1989.  
XX  
XX 21-OCT-1988; 88EP-00309907.  
XX  
XX 23-OCT-1987; 87US-00112800.  
XX  
XX (SMIK ) SMITHKLINE BECKMAN CORP.  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX PI Deen KC, Polenawaas GM, Inacker RH, Sweet RW;  
XX  
XX WPI; 1989-124209/17.  
XX N-PSDB; AAN90763.  
XX  
XX Purifying soluble recombinant T4 lymphocyte surface protein - from cell  
XX culture by adsorption on cation exchanger, elution and treatment with  
XX anion exchanger.  
XX  
XX Disclosure; Fig 1; 13pp; English.  
XX  
XX The coding sequence is derived from the published sequence of sT4. sT4 is  
XX useful in the prevention and treatment of AIDS by inhibiting spread of  
XX the virus. It can also be used as an inhibitor of T4+ cell function, as a  
XX reagent for identifying inhibitors of T4+ cell interaction and to produce

CC diagnostic monoclonal antibodies. (updated on 25-MAR-2003 to correct PA  
CC field.) (Updated on 25-MAR-2003 to correct PI field.)  
XX  
XX  
SO Sequence 394 AA;  
Query Match 77.9%; Score 1026; DB 1; Length 394;  
Best Local Similarity 99.5%; Pred. No. 2,5e-63;  
Matches 199; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNRGVPFRHLVLTALPAATQGNKVLTGKKGDTVELTCTASOKKSTIOFHKNSNOIK 60  
DB 1 MNRGVPFRHLVLTALPAATQGNKVLTGKKGDTVELTCTASOKKSTIOFHKNSNOIK 60  
QY 61 ILGNQGSFLTKGPSKLTNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEYVL 120  
DB 61 ILGNQGSFLTKGPSKLTNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEYVL 120  
QY 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPSVQCRSPRGKNIQGKTLVSQLEIQDSG 180  
DB 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPSVQCRSPRGKNIQGKTLVSQLEIQDSG 180  
QY 181 TWTCTVLQONOKKVEPKIDIV 200  
DB 181 TWTCTVLQONOKKVEPKIDIV 200  
RESULT 53  
AAE37197  
ID AAE37197 standard; protein; 202 AA.  
XX AAE37197;  
AC 07-AUG-2003 (first entry)  
DT  
XX  
XX  
DE sCD4 protein.  
XX  
XX CD4-inducible epitope; Human immunodeficiency virus; HIV; gene therapy;  
XX HIV infection; envelope glycoprotein; Env; vaccine; sCD4.  
XX  
XX Unidentified.  
XX  
XX WO2003033666-A2.  
XX  
XX 24-APR-2003.  
XX  
XX 16-OCT-2002; 2002WO-US033165.  
XX  
XX 16-OCT-2001; 2001US-0329709P.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Dimitrov DS, Moulard M, Xiao X, Shu Y, Phogat SK, Zhang M;  
XX Burton D;  
XX  
XX WPI; 2003-393518/37.  
XX  
XX  
XX New isolated antibody or antibody fragment specifically binds a CD4-  
XX inducible epitope on Human Immunodeficiency Virus (HIV) Env proteins,  
XX useful for preparing a composition for treating or preventing HIV  
XX infection.  
XX  
XX Example 3; Page 33; 69pp; English.  
XX  
XX The invention relates to antibodies or antibody fragments specifically  
XX binding to CD4-inducible epitope on Human immunodeficiency virus (HIV)  
XX envelope glycoprotein (Env) proteins. The antibody is useful for  
XX preparing a composition for treating or preventing HIV infection. The  
XX invention is used to prepare vaccines and is used in gene therapy. The  
XX present sequence is a sCD4 protein used in the exemplification of the  
XX invention  
XX  
XX Sequence 202 AA;

```
Query Match          77.7%; Score 1023; DB 6; Length 202;
Best Local Similarity 99.5%; Pred. No. 1.9e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPPRHLLVLTQLALPPAATQGNKVLGKKGDVVELTCTASOKKSIQFHWKNSNQIK 60
DB 1 MNRGVPPRHLLVLTQLALPPAATQGNKVLGKKGDVVELTCTASOKKSIQFHWKNSNQIK 60
QY 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSGLTLTLSPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSGLTLTLSPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNGKKEFKIDIV 200
DB 181 TWTCTVLQNGKKEFKIDIV 200

RESULT 54
AAR07605
ID AAR07605 standard; protein; 295 AA.
XX
AC AAR07605;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 06-FEB-1991 (first entry)
XX
DE Plasmid T4/LFA-3/AD gene product with C-terminal encoding
DE phosphatidylinositol (PI) linkage signaling sequence.
XX
KM Plasma membrane binding affinity; micelle.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Protein 1..266
FT Peptide 267..295
FT Peptide /label= PI signal peptide
XX
PN W09012099-A.
PD 18-OCT-1990.
XX
PF 10-APR-1989; 89US-00335688.
XX
PR 10-APR-1989; 89US-00335688.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Wallner BP;
XX
DR WPI; 1990-334849/44.
DR N-PSDB; AAQ06404.
XX
PT Phosphatidyl-inositol linkage signalling DNA sequence - derived from
PT lymphocyte function-associated antigen 3, used for prodn. of chimeric
PT proteins.
XX
PS Disclosure; Fig 4; 53pp; English.
XX
CC The signal sequence is attached downstream of the plasmid sequence
CC encoding a secreted protein, which will then produce proteins covalently
CC anchored to the cell surface in which they were produced. This can give
CC rise to plasma membrane binding, enhanced purifiability, micelle
CC formation etc. especially useful in the production of chimeric targeted
CC drugs, to produce micellar or liposomal delivery systems or in enhanced
CC purification and screening of cells, proteins or DNA libraries. (Updated
```

```
CC on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 295 AA;
Query Match          77.7%; Score 1023; DB 2; Length 295;
Best Local Similarity 99.5%; Pred. No. 3e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPPRHLLVLTQLALPPAATQGNKVLGKKGDVVELTCTASOKKSIQFHWKNSNQIK 60
DB 1 MNRGVPPRHLLVLTQLALPPAATQGNKVLGKKGDVVELTCTASOKKSIQFHWKNSNQIK 60
QY 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSGLTLTLSPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSGLTLTLSPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNGKKEFKIDIV 200
DB 181 TWTCTVLQNGKKEFKIDIV 200

RESULT 55
AAR07606
ID AAR07606 standard; protein; 318 AA.
XX
AC AAR07606;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 06-FEB-1991 (first entry)
XX
DE Plasmid T4/LFA-3/2 gene product with C-terminal encoding
DE phosphatidylinositol (PI) linkage signaling sequence.
XX
KM Plasma membrane binding affinity; micelle.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Protein 1..267
FT Peptide 267..318
FT Peptide /label= LFA-3 gene product
FT Peptide /label= PI signal peptide
XX
PN W09012099-A.
PD 18-OCT-1990.
XX
PF 10-APR-1989; 89US-00335688.
XX
PR 10-APR-1989; 89US-00335688.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Wallner BP;
XX
DR WPI; 1990-334849/44.
DR N-PSDB; AAQ06405.
XX
PT Phosphatidyl-inositol linkage signalling DNA sequence - derived from
PT lymphocyte function-associated antigen 3, used for prodn. of chimeric
PT proteins.
XX
PS Disclosure; Fig 5; 53pp; English.
XX
CC The signal sequence is attached downstream of the plasmid sequence
CC encoding a secreted protein, which will then produce proteins covalently
CC anchored to the cell surface in which they were produced. This can give
```

CC rise to plasma membrane binding, enhanced purifiability, micelle  
 CC formation etc. especially useful in the production of chimeric targeted  
 CC drugs, to produce micellar or liposomal delivery systems or in enhanced  
 CC purification and screening of cells, proteins or DNA libraries. (Updated  
 CC on 03-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to  
 CC correct PA field.)

XX  
 SQ Sequence 318 AA;

Query Match 77.7%; Score 1023; DB 2; Length 318;  
 Best Local Similarity 99.5%; Pred. No. 3.2e-63;  
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKKGDVLTCTASQKSIQPFHKNKNQIK 60  
 DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKKGDVLTCTASQKSIQPFHKNKNQIK 60  
 QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVDQKEEVQL 120  
 DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVDQKEEVQL 120  
 QY 121 LVFGLTANSDTHLLOQGSLLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGLTANSDTHLLOQGSLLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 QY 181 TWTCTVLQNKVKVEFKIDIV 200  
 DB 181 TWTCTVLQNKVKVEFKIDIV 200

RESULT 56  
 AAY39825  
 ID AAY39825 standard; protein; 394 AA.

XX AAY39825;

XX 03-DEC-1999 (first entry)

XX Soluble human T4 protein.

KM Soluble T4 protein; sT4; human; HIV; binding inhibitor; T4+ cell; AIDS;  
 KM vaccine; immunisation; therapy.

XX Homo sapiens.

XX USS958678-A.

XX 28-SEP-1999.

XX 12-DEC-1994; 94US-00354452.

XX 21-AUG-1986; 86US-00898587.

PR 11-JUN-1991; 91US-00713564.

PR 06-JUL-1992; 92US-00909021.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Mcdougal JS, Weiss R, Axel R, Littman DR, Maddon PJ, Chess L,

XX WPI; 1999-561025/47.

XX N-PSDB; AAZ20694.

XX Human T4 protein inhibits HIV binding to T4 cells, useful for treating

XX AIDS.

XX Disclosure; Col 13-16; 58pp; English.

XX This sequence represents the soluble human T4 protein of the invention.  
 CC The soluble human T4 protein blocks the binding of HIV to T4+ cells and  
 CC is therefore useful for the treatment of AIDS. Monoclonal antibodies  
 CC against the T4 protein may be used as vaccines for immunising subjects  
 CC against AIDS

SQ Sequence 394 AA;

Query Match 77.7%; Score 1023; DB 2; Length 394;  
 Best Local Similarity 99.5%; Pred. No. 4.1e-63;  
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKKGDVLTCTASQKSIQPFHKNKNQIK 60  
 DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKKGDVLTCTASQKSIQPFHKNKNQIK 60  
 QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVDQKEEVQL 120  
 DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVDQKEEVQL 120  
 QY 121 LVFGLTANSDTHLLOQGSLLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGLTANSDTHLLOQGSLLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 QY 181 TWTCTVLQNKVKVEFKIDIV 200  
 DB 181 TWTCTVLQNKVKVEFKIDIV 200

RESULT 57  
 AAY88328  
 ID AAY88328 standard; protein; 394 AA.

XX AAY88328;

XX 14-JUL-2000 (first entry)

XX T4 glycoprotein amino acid sequence.

KM sT4; glycoprotein; human immunodeficiency virus; HIV; block binding;  
 KM AIDS; treatment; inhibic; cell to cell spread; infection; fusion.

XX Mammalia.

XX USS126433-A.

XX 30-JUN-1992.

XX 23-OCT-1987; 87US-00114244.

XX 21-AUG-1986; 86US-00898587.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Maddon PJ, Chess L, Weiss R, Littman DR, Mcdougal JS;

XX WPI; 2000-348913/30.

XX N-PSDB; AAA10906.

XX Soluble T4 glycoprotein useful for prevention and treatment of acquired  
 PT immunodeficiency syndrome and for screening inhibitors of human  
 PT immunodeficiency viral binding.

XX Disclosure; Col 11-16; 64pp; English.

XX This sequence represents the full length amino acid sequence of  
 CC glycosylated sT4 glycoprotein. Human immunodeficiency virus (HIV) uses  
 CC sT4 as a target receptor on T cells. The invention relates to  
 CC glycosylated sT4 which functions by blocking the binding of HIV to T4  
 CC target cells, and can be used for the prophylaxis and treatment of AIDS  
 CC patients. Administration of sT4 effectively inhibits the cell to cell  
 CC spreading of HIV infection and also the fusion of HIV-infected T4 cells  
 CC and non-infected T4 cells. The administration of T4 alleviates several  
 CC symptoms associated with AIDS. The administration of T4 alleviates several  
 CC pathological changes. The sT4 glycoprotein is useful for the prophylaxis  
 CC and treatment of patients with AIDS. It is also useful as a reagent to  
 CC identify natural, synthetic or recombinant molecules which act as  
 CC therapeutic agents or inhibitors of T4 cell interactions and in  
 CC diagnostic assays for detection T4 proteins or molecules

XX Sequence 394 AA;  
 SQ Query Match 77.7%; Score 1023; DB 3; Length 394;  
 Best Local Similarity 99.5%; Pred. No. 4.1e-63;  
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MNRGVPRHLLLVQLALPAATQGNKVVLGKKGDVVELCTASQKKSIOFHWKNSNQIK 60  
 1 MNRGVPRHLLLVQLALPAATQGNKVVLGKKGDVVELCTASQKKSIOFHWKNSNQIK 60  
 Db 1 MNRGVPRHLLLVQLALPAATQGNKVVLGKKGDVVELCTASQKKSIOFHWKNSNQIK 60

QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEVOL 120  
 Db 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEVOL 120

QY 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCSPRGKNIQGGKTLVSQLELDQSG 180  
 Db 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCSPRGKNIQGGKTLVSQLELDQSG 180

QY 181 TWCTVLOQOKKVEFKIDIV 200  
 Db 181 TWCTVLOQOKKVEFKIDIV 200

RESULT 58  
 AAB19509 ID AAB19509 standard; protein; 416 AA.  
 XX AAB19509;  
 AC AAB19509;  
 DT 09-JAN-2001 (first entry)  
 XX  
 DE CD4-IgM fusion protein CH4Mmu.  
 XX  
 KM CD4; IgM; human; CD4Mmu; fusion protein; immunoglobulin; HIV; SIV; gp120;  
 KM therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 1..395  
 FT /note= "CD4 extracellular region"  
 FT Protein 400..416  
 FT /note= "IgM heavy chain partial sequence"  
 XX  
 PN US6117656-A.  
 XX  
 XX 12-SEP-2000.  
 PD  
 XX  
 PF 07-JUN-1995; 95US-00479353.  
 XX  
 XX 22-JAN-1988; 88US-00147351.  
 PR 23-JAN-1989; 89US-00299596.  
 PR 09-JUN-1992; 92US-00896781.  
 PR 12-APR-1993; 93US-00057952.  
 PR 04-FEB-1994; 94US-00191708.  
 XX  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA  
 XX  
 PI Seed B;  
 XX  
 DR WPI; 2000-586558/55.  
 DR N-PSDB; AAA50662.  
 XX  
 PT CD4-Immunoglobulin fusion proteins, useful for targeting gp120 of HIV or  
 PT SIV.  
 XX  
 PS Example 1; Col 41-50; 39pp; English.  
 XX  
 CC The present sequence is that of fusion protein CD4Mmu comprising the  
 CC extracellular portion of CD4, which binds to HIV gp120, linked at its C-  
 CC terminus to the human IgM heavy chain. To obtain the fusion protein, DNA  
 CC encoding CD4 was linked to IgM DNA at the Met2 site upstream of the CH1

CC region (see AAA50662). Fusion protein CD4Mmu and a nucleic acid encoding  
 CC it are claimed. Also claimed are a vector comprising the nucleic acid,  
 CC and a method of producing the fusion protein in secreted form using a  
 CC transformed host cell. The fusion protein may further comprise a  
 CC therapeutic agent, radiolabel or NMR imaging agent. The fusion protein  
 CC can be administered to an animal (including humans) for treatment of HIV  
 CC or SIV infection, and can also be used in assays for HIV or SIV, imaging  
 CC and tissue stains. IgM fusion proteins such as CD4Mmu provide complement-  
 CC mediated immunity  
 XX  
 SQ Sequence 416 AA;  
 Query Match 77.7%; Score 1023; DB 3; Length 416;  
 Best Local Similarity 99.5%; Pred. No. 4.3e-63;  
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MNRGVPRHLLLVQLALPAATQGNKVVLGKKGDVVELCTASQKKSIOFHWKNSNQIK 60  
 1 MNRGVPRHLLLVQLALPAATQGNKVVLGKKGDVVELCTASQKKSIOFHWKNSNQIK 60  
 Db 1 MNRGVPRHLLLVQLALPAATQGNKVVLGKKGDVVELCTASQKKSIOFHWKNSNQIK 60

QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEVOL 120  
 Db 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEVOL 120

QY 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCSPRGKNIQGGKTLVSQLELDQSG 180  
 Db 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCSPRGKNIQGGKTLVSQLELDQSG 180

QY 181 TWCTVLOQOKKVEFKIDIV 200  
 Db 181 TWCTVLOQOKKVEFKIDIV 200

RESULT 59  
 AAY51080 ID AAY51080 standard; protein; 436 AA.  
 XX AAY51080;  
 AC AAY51080;  
 DT 23-MAR-2000 (first entry)  
 XX  
 DE Human fusion protein CD4Mg.  
 XX  
 KM Fusion protein; human; CD4; IgM; immunoglobulin; gp120;  
 KM anti-human immunodeficiency virus; CD4Mg.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US6004761-A.  
 XX  
 XX 21-DEC-1999.  
 PD  
 XX  
 PF 04-FEB-1994; 94US-00191708.  
 XX  
 XX 22-JAN-1988; 88US-00147351.  
 PR 23-JAN-1989; 89US-00299596.  
 PR 09-JUN-1992; 92US-00896781.  
 PR 12-APR-1993; 93US-00057952.  
 XX  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA  
 XX  
 PI Seed B;  
 XX  
 DR WPI; 2000-085792/07.  
 DR N-PSDB; AA244063.  
 XX  
 PT Fusion protein useful for the treatment of human immunodeficiency virus.  
 PT  
 XX  
 PS Example 1; Col 41-50; 39pp; English.  
 XX  
 CC This invention describes a novel nucleic acid (I) encoding a fusion  
 CC protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)

CC and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products of the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4mg which is constructed from CD4 linked to human Igm upstream of the CH1 region

SO Sequence 436 AA;

Query Match 77.7%; Score 1023; DB 3; Length 436;  
Best Local Similarity 99.5%; Pred. No. 4.6e-63;  
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRGVPRHLVLTALLPAATQGNKVVLGKGDVETCTASQKSIQPFHKNNOIK 60  
DB 1 MKRGVPRHLVLTALLPAATQGNKVVLGKGDVETCTASQKSIQPFHKNNOIK 60  
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEVQL 120  
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEVQL 120  
QY 121 LVFGILTANSDTHLLOGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELODSG 180  
DB 121 LVFGILTANSDTHLLOGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELODSG 180  
QY 181 TWTCTVLONQKVEFKIDIV 200  
DB 181 TWTCTVLONQKVEFKIDIV 200

RESULT 60

AAY88329  
ID AAY88329 standard; protein; 458 AA.

XX AAY88329;

DT 14-JUL-2000 (first entry)

DE T4 glycoprotein amino acid sequence.

KW sT4; glycoprotein; human immunodeficiency virus; HIV; block binding;  
KM AIDS; treatment; inhibit; cell to cell spread; infection; fusion.

OS Mammalia.

PN US5126433-A.

PD 30-JUN-1992.

PF 23-OCT-1987; 87US-00114244.

PR 21-AUG-1986; 86US-00896587.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Madden PJ, Chess L, Axel R, Weiss R, Littman DR, McDougal JS;

DR WPI; 2000-348913/30.

PT Soluble T4 glycoprotein useful for prevention and treatment of acquired immunodeficiency syndrome and for screening inhibitors of human immunodeficiency viral binding.

PS Example; Fig 6; 64pp; English.

CC This sequence represents the amino acid sequence of glycosylated sT4 glycoprotein. Human immunodeficiency virus (HIV) uses sT4 as a target receptor on T cells. The invention relates to glycosylated sT4 which functions by blocking the binding of HIV to T4 target cells, and can be used for the prophylaxis and treatment of AIDS patients. Administration of sT4 effectively inhibits the cell to cell spreading of HIV infection and also the fusion of HIV-infected T4 cells and non-infected T4 cells.

CC The administration of T4 alleviates several symptoms associated with AIDS, and prevents the occurrence of new pathological changes. The sT4 glycoprotein is useful for the prophylaxis and treatment of patients with AIDS. It is also useful as a reagent to identify natural, synthetic or recombinant molecules which act as therapeutic agents or inhibitors of T4 cell interactions and in diagnostic assays for detection T4 proteins or molecules

SO Sequence 458 AA;

Query Match 77.7%; Score 1023; DB 3; Length 458;  
Best Local Similarity 99.5%; Pred. No. 4.8e-63;  
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRGVPRHLVLTALLPAATQGNKVVLGKGDVETCTASQKSIQPFHKNNOIK 60  
DB 1 MKRGVPRHLVLTALLPAATQGNKVVLGKGDVETCTASQKSIQPFHKNNOIK 60  
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEVQL 120  
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEVQL 120  
QY 121 LVFGILTANSDTHLLOGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELODSG 180  
DB 121 LVFGILTANSDTHLLOGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELODSG 180  
QY 181 TWTCTVLONQKVEFKIDIV 200  
DB 181 TWTCTVLONQKVEFKIDIV 200

RESULT 61

AAB81502  
ID AAB81502 standard; protein; 458 AA.

XX AAB81502;

DT 18-JUN-2001 (first entry)

DE Human CD4 protein.

KW Human; CD4; CD4 fusion protein; oligomerisation;  
KM receptor-ligand interaction inhibition; surface plasmon resonance; SPR;  
KW T cell receptor binding; MHC binding; carcinoma; autoimmune disease;  
KM multiple sclerosis; human immunodeficiency virus; HIV; diabetes;  
KW rheumatoid arthritis; immune disorder.

OS Homo sapiens.

PN

PD

PF

PR

PI

DR

PT Key Location/Qualifiers  
1..25  
/label= Signal\_peptide  
26..458  
/label= Human\_CD4

MO200122084-A2.

PD 29-MAR-2001.

PF 18-SEP-2000; 2000WO-GB003579.

PR 21-SEP-1999; 99GB-00022352.

PA (AVID-) AVIDEX LTD.  
PI Jakobsen BK;  
XX WPI; 2001-273470/28.  
DR N-PSDB; AAF82582.  
PT Sequential screening of candidate compounds library for those which inhibit binding of low affinity receptor-ligand interaction having fast binding kinetics, using interfacial optical assay.



XX	PS	Discloure; Fig 13; 91pp; English.
XX	XX	
CC	CC	The present sequence is human CD4. Human CD4 extracellular domains 1 and
CC	CC	2 were used in the construction of CD4 oligomerisation fusion proteins.
CC	CC	The fusion proteins contain an oligomerisation domain that enables the
CC	CC	proteins to bind to one another to form oligomers. The oligomers may be
CC	CC	used in an invention relating to a method for screening for compounds
CC	CC	with the ability to inhibit a low affinity receptor-ligand interaction.
CC	CC	The method uses an interfacial optical assay, such as surface plasmon
CC	CC	resonance (SPR). The method is useful for screening candidate compounds
CC	CC	for the ability to inhibit interaction between MHC/peptide complex and T
CC	CC	cell receptor, and MHC/peptide complex and CD8 or CD4 co-receptor. The
CC	CC	compound identified by the above methods which interfere with T cell
CC	CC	receptor binding to a particular HLA type molecule are useful as immune
CC	CC	inhibitors for treating carcinomas, autoimmune diseases such as multiple
CC	CC	sclerosis, human immunodeficiency virus (HIV) infection, rheumatoid
CC	CC	arthritis, Hashimoto's disease, insulin dependent diabetes, Good
CC	CC	pasture's syndrome, uveitis, psoriasis and graft rejection
XX	XX	
XX	XX	Sequence 458 AA;
XX	XX	
QY	QY	Query Match 77.7%; Score 1023; DB 4; Length 458;
Db	Db	Best Local Similarity 99.5%; Pred. No. 4,8e-63;
		Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	QY	1 MNRGVFPHLLLVLDLALLPAATQGNKVVLGKKGDVLTCTASQKKSIOFHWKNSNOIK 60
Db	Db	1 MNRGVFPHLLLVLDLALLPAATQGNKVVLGKKGDVLTCTASQKKSIOFHWKNSNOIK 60
QY	QY	61 ILGNQGSFLTYKGPSKLTNDRAISRSLMNOGNPRLIIKLIKIDSTYICVVDQKEEYQL 120
Db	Db	61 ILGNQGSFLTYKGPSKLTNDRAISRSLMNOGNPRLIIKLIKIDSTYICVVDQKEEYQL 120
QY	QY	121 LVFGILTASDPHLLLOGQS/TLTLESPPSSPSPVQCRSPRGKNIQSGKTLVSQLELDPSG 180
Db	Db	121 LVFGILTASDPHLLLOGQS/TLTLESPPSSPSPVQCRSPRGKNIQSGKTLVSQLELDPSG 180
QY	QY	181 TWTCVTVLQNOKKVEFKIDIV 200
Db	Db	181 TWTCVTVLQNOKKVEFKIDIV 200
XX	XX	
XX	XX	RESULT 62
XX	XX	AAG79087
XX	XX	ID AAG79087 standard; protein; 458 AA.
XX	XX	AC AAG79087;
XX	XX	DT 10-DEC-2001 (first entry)
XX	XX	DE Amino acid sequence of human CD4 protein.
XX	XX	KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
XX	XX	XX C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CD4.
XX	XX	OS Homo sapiens.
XX	XX	PN WO200164752-A2.
XX	XX	PD 07-SEP-2001.
XX	XX	PF 28-FEB-2001; 2001WO-US006322.
XX	XX	02-MAR-2000; 2000US-00517605.
XX	XX	(UYNV ) UNIV NEW YORK STATE.
XX	XX	PA (UYNV-) UNIV NIJMEGEN.
XX	XX	PI Litman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
XX	XX	WI; 2001-602565/68.

[illegible]

XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
PI WPI; 2003-801317/75.  
XX  
XX New binding domain-immunoglobulin fusion protein, useful for treating a  
PT subject having or suspected of having a malignant condition or a B-cell  
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
XX  
XX Disclosure; SEQ ID NO 170; 157pp; English.  
XX  
XX The invention relates to a binding domain-immunoglobulin fusion protein  
CC comprising a binding domain polypeptide that is fused to an  
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
CC CH2 constant region polypeptide that is fused to the hinge region  
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
CC polypeptide that is fused to the CH2 constant region polypeptide. The  
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin  
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
CC region polypeptide, derived from (a) having 3 or more cysteine residues;  
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
CC immunoglobulin hinge region polypeptide contains no more than one  
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region  
CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
CC capable of at least one immunological activity comprising antibody  
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
CC binding domain polypeptide is capable of specifically binding to an  
CC antigen. Also included are an isolated polynucleotide encoding the  
CC binding domain-immunoglobulin fusion protein, a recombinant expression  
CC construct comprising the polynucleotide (operably linked to a promoter),  
CC a host cell transformed or transfected with a recombinant expression  
CC construct, producing the binding domain-immunoglobulin fusion protein, a  
CC pharmaceutical composition comprising the binding domain-immunoglobulin  
CC fusion protein or polynucleotide and a carrier, and treating a subject  
CC having or suspected of having a malignant condition or a B-cell disorder.  
CC The binding domain-immunoglobulin fusion protein is useful for treating a  
CC subject having or suspected of having a malignant condition or a B-cell  
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
CC sclerosis or autoimmune disease. The present sequence is a binding domain  
CC -immunoglobulin fusion protein-associated protein sequence. Note: The  
CC sequence data for this patent formed part of the printed specification  
CC and is also available in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not  
CC identified the sequences in the printed specification by their SEQ ID  
CC number therefore none of the sequences can be explicitly identified.  
XX  
XX Sequence 458 AA:  
SQ  
Query Match 77.7%; Score 1023; DB 7; Length 458;  
Best Local Similarity 99.5%; Pred. No. 4.8e-63;  
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MANGVPRHLLVLTQALLPAATQGNKVYLGKGDYVELTCTASOKKSIOPHKNKNQIK 60  
DB 1 MANGVPRHLLVLTQALLPAATQGNKVYLGKGDYVELTCTASOKKSIOPHKNKNQIK 60  
QY 1LNGGSLFKTGPSKLNDRADSRSLWDQGNPFLITKNLKIIESDPYICEVEQKEEVOL 120  
DB 61 ILNGGSLFKTGPSKLNDRADSRSLWDQGNPFLITKNLKIIESDPYICEVEQKEEVOL 120  
QY 1LVFGLTANSPTHLIQGSLTILTESPPGSSPVQCSPRGKNIQGGKTISSVSLQLEIDQSG 180  
DB 121 LVFGLTANSPTHLIQGSLTILTESPPGSSPVQCSPRGKNIQGGKTISSVSLQLEIDQSG 180  
QY 181 TWTCVTQONOKVVEFKIDIV 200  
DB 181 TWTCVTQONOKVVEFKIDIV 200

RESULT 64  
AD57489  
ID AD57489 standard; protein; 458 AA.  
XX  
XX AD57489;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Human Protein P01730, SEQ ID NO 3351.  
DE  
XX  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003016475-A2.  
PN  
XX  
XX 27-FEB-2003.  
PD  
XX  
XX 14-AUG-2002; 2002MO-US025765.  
PF  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR  
XX  
XX 01-NOV-2001; 2001US-0346382P.  
PR  
XX  
XX 26-NOV-2001; 2001US-0333347P.  
PR  
XX  
XX (GENO) GEN HOSPITAL CORP.  
PA  
XX  
XX (FARB) BAYER AG.  
PI  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
PI WPI: 2003-268312/26.  
DR  
XX  
XX GENBANK; P01730.  
DR  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX  
XX  
XX Claim 1, Page; 1017pp; English.  
PS  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a  
XX method for identifying a compound or small molecule that regulates the  
XX activity in an animal of one or more of the polypeptides given in the  
XX specification, a method for identifying a compound useful in treating  
XX pain and a pharmaceutical composition comprising the one or more  
XX polypeptides or their antibodies. The polynucleotide or the compound that  
XX modulates its activity is useful for preparing a medicament for treating  
XX pain (e.g. spinal segmental nerve injury (SNI), chronic constriction  
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
XX therapy). The sequence presented is a human protein (shown in Table 2 of  
XX the specification) which is differentially expressed during pain. Note:  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic form directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
SQ  
Sequence 458 AA:  
SQ  
Query Match 77.7%; Score 1023; DB 7; Length 458;  
Best Local Similarity 99.5%; Pred. No. 4.8e-63;

Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MNRGVPRRHLLVLTQALLPAAATGKNKVLGKKDVTVELTCTAQSOKKSIOFHKNNSQIK 60
DB 1 MNRGVPRRHLLVLTQALLPAAATGKNKVLGKKDVTVELTCTAQSOKKSIOFHKNNSQIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOQGSILTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSILTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWCTCTVLQNKVKVEFKIDIV 200
DB 181 TWCTCTVLQNKVKVEFKIDIV 200

```

## RESULT 65

ADA44807  
ID ADA44807 standard; protein; 473 AA.

AC ADA44807;  
DT 04-DEC-2003 (first entry)

DE CD4/TCR CD3epsilon chain chimeric protein CD4epsilon15, SEQ ID NO:2.

KW HIV-1 infection; human immunodeficiency virus-1; CD4+ cell; chimeric CD4;

KM endoplasmic reticulum; ER retention; envelope protein gp160;

KW T cell receptor CD3epsilon chain; C-terminal domain; CD4epsilon15;

KW gene therapy; human; receptor.

OS Chimeric.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

CC expression system encoding a chimeric CD4 protein. The ER-localised  
CC chimeric CD4 molecule binds to the HIV-1 envelope protein gp160,  
CC resulting in HIV-1 retention in the ER and thereby preventing viral  
CC replication. In a specific embodiment, the chimeric CD4 molecule  
CC comprises CD4 fused to 15 amino acids of the C-terminal domain of the T  
CC cell receptor CD3epsilon chain; this chimeric CD4 molecule is designated  
CC CD4epsilon15 (ADA44807). A known chimeric CD4 of similar structure but  
CC containing only 10 amino acids from CD3epsilon can also be used.  
CC Compositions of the invention have an in trans effect on the replication  
CC of HIV-1, and may be used to treat and prevent HIV-1 infection. The  
CC present sequence represents the chimeric CD4 molecule CD4epsilon15, which  
CC is specifically claimed for use in compositions of the invention.

XX Sequence 473 AA.

Query Match 77.7%; Score 1023; DB 7; Length 473;  
Best Local Similarity 99.5%; Pred. No. 5e-63;  
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MNRGVPRRHLLVLTQALLPAAATGKNKVLGKKDVTVELTCTAQSOKKSIOFHKNNSQIK 60
DB 1 MNRGVPRRHLLVLTQALLPAAATGKNKVLGKKDVTVELTCTAQSOKKSIOFHKNNSQIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOQGSILTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSILTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWCTCTVLQNKVKVEFKIDIV 200
DB 181 TWCTCTVLQNKVKVEFKIDIV 200

```

## RESULT 66

AA59170  
ID AA59170 standard; protein; 474 AA.

AC AA59170;

DT 14-MAR-2000 (first entry)

DE CD4-Ig fusion protein CD4Mmu.

KW HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;

KW secreted protein; SIV infection; medicament.

OS Synthetic.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

The invention provides a fusion gene encoding a fusion protein that

CC comprises an extracellular CD4 DNA sequence or its fragment which binds  
 CC to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA  
 CC sequence of an Ig heavy or light chain, where the DNA sequence encoding  
 CC the variable region has been replaced with the DNA sequence which encodes  
 CC extracellular CD4 or its gp120 binding fragment. The fusion protein is  
 CC capable of being secreted. The fusion proteins are useful for treating  
 CC HIV or SIV infections in animals, preferably humans. They are also useful  
 CC for producing medicaments which can be used for treating HIV or SIV  
 CC infections in humans. The present sequence represents the fusion protein  
 CC CD4muu where the CD4 is linked to human IgG1 at the Met2 site upstream of  
 CC the CH1 region  
 XX  
 SQ Sequence 474 AA;  
 Query Match 77.7%; Score 1023; DB 3; Length 474;  
 Best Local Similarity 99.5%; Pred. No. 5e-63; Indels 0; Gaps 0;  
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MNRGVPFRHLVLQALLPATQGNKVVYLGKKGDTVELTCTASQKKSIOFHMKNSNOIK 60  
 DB 1 MNRGVPFRHLVLQALLPATQGNKVVYLGKKGDTVELTCTASQKKSIOFHMKNSNOIK 60  
 QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLKIENSDTYICEVEDQKEEYQL 120  
 DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLKIENSDTYICEVEDQKEEYQL 120  
 QY 121 LVFGILTANSDTHLLQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGILTANSDTHLLQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 QY 181 TWTCTVLOQOKKVEFKIDIV 200  
 DB 181 TWTCTVLOQOKKVEFKIDIV 200  
 RESULT 67  
 AAB19510  
 ID AAB19510 standard; protein; 481 AA.  
 XX  
 AC AAB19510;  
 XX  
 DT 09-JAN-2001 (first entry)  
 XX  
 DE CD4-IgM fusion protein CH4Pmu.  
 XX  
 KM CD4; IgM; human; CD4Pmu; fusion protein; immunoglobulin; HIV; SIV; gp120;  
 KM therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Protein 1..395  
 FT Protein /note="CD4 extracellular region"  
 FT Protein 400..481  
 FT Protein /note="IgM heavy chain partial sequence"  
 XX  
 PN US6117656-A.  
 XX  
 PD 12-SEP-2000.  
 XX  
 PF 07-JUN-1995; 95US-00479353.  
 XX  
 XX 22-JAN-1988; 88US-00147351.  
 PR 23-JAN-1989; 89US-00299596.  
 PR 09-JUN-1992; 92US-00896781.  
 PR 12-APR-1993; 93US-00057952.  
 PR 04-FEB-1994; 94US-00191708.  
 XX  
 XX (GEHO ) GEN HOSPITAL CORP.  
 XX  
 XX Seed B;  
 XX  
 XX WPI; 2000-586558/55.  
 DR

DR N-PSDB; AAB50662.  
 XX  
 XX CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV or  
 PT SIV.  
 XX  
 XX Example 1, Col 49-60; 39pp; English.  
 PS  
 XX The present sequence is that of fusion protein CD4Pmu comprising the  
 XX extracellular portion of CD4, which binds to HIV gp120, linked at its C-  
 CC terminus to the human IgM heavy chain. To obtain the fusion protein, DNA  
 CC encoding CD4 was linked to IgM DNA at the Pst site upstream of the CH2  
 CC region (see AAB50663). Fusion protein CD4Pmu and a nucleic acid encoding  
 CC it are claimed. Also claimed are a vector comprising the nucleic acid,  
 CC and a method of producing the fusion protein in secreted form using a  
 CC transformed host cell. The fusion protein may further comprise a  
 CC therapeutic agent, radiolabel or NMR imaging agent. The fusion protein  
 CC can be administered to an animal (including humans) for treatment of HIV  
 CC or SIV infection, and can also be used in assays for HIV or SIV, imaging  
 CC and tissue stains. IgM fusion proteins such as CD4Pmu provide complement-  
 CC mediated immunity  
 XX  
 SQ Sequence 481 AA;  
 Query Match 77.7%; Score 1023; DB 3; Length 481;  
 Best Local Similarity 99.5%; Pred. No. 5.1e-63; Indels 0; Gaps 0;  
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MNRGVPFRHLVLQALLPATQGNKVVYLGKKGDTVELTCTASQKKSIOFHMKNSNOIK 60  
 DB 1 MNRGVPFRHLVLQALLPATQGNKVVYLGKKGDTVELTCTASQKKSIOFHMKNSNOIK 60  
 QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLKIENSDTYICEVEDQKEEYQL 120  
 DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLKIENSDTYICEVEDQKEEYQL 120  
 QY 121 LVFGILTANSDTHLLQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGILTANSDTHLLQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 QY 181 TWTCTVLOQOKKVEFKIDIV 200  
 DB 181 TWTCTVLOQOKKVEFKIDIV 200  
 RESULT 68  
 AAB51081  
 ID AAB51081 standard; protein; 481 AA.  
 XX  
 AC AAB51081;  
 XX  
 DT 23-MAR-2000 (first entry)  
 XX  
 DE Human fusion protein CD4Pmu.  
 XX  
 KM Fusion protein; human; CD4; IgM; immunoglobulin; gp120;  
 KM anti-human immunodeficiency virus; CD4Pmu.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US6004781-A.  
 XX  
 PD 21-DEC-1999.  
 XX  
 XX 04-FEB-1994; 94US-00191708.  
 PR 22-JAN-1988; 88US-00147351.  
 PR 23-JAN-1989; 89US-00299596.  
 PR 09-JUN-1992; 92US-00896781.  
 PR 12-APR-1993; 93US-00057952.  
 XX  
 XX (GEHO ) GEN HOSPITAL CORP.  
 XX  
 XX

PI Seed B;  
 XX WPI: 2000-085792/07.  
 DR N-PSDB: AA244064.  
 XX  
 XX Fusion protein useful for the treatment of human immunodeficiency virus.  
 PS Example 1; Col 49-58; 39pp; English.  
 XX  
 CC This invention describes a novel nucleic acid (I) encoding a fusion  
 CC protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)  
 CC and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light  
 CC chain (III). The products of the invention have anti-human  
 CC immunodeficiency virus (HIV) activity and are capable of binding to  
 CC gp120. The fusion protein is useful for treating human immunodeficiency  
 CC virus (HIV) or simian immunodeficiency virus (SIV). This sequence  
 CC represents the fusion protein CD4Pmu which is constructed from CD4 linked  
 CC to human Igm upstream of the CH2 region  
 XX  
 SQ Sequence 481 AA;

Query Match 77.7%; Score 1023; DB 3; Length 481;  
 Best Local Similarity 99.5%; Pred. No. 5.1e-63;  
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNRGVPFRHLVLVQLALPPAATQGNKVVLGKGGDTVELTCTASOKKSIOPFMKNSNOIK 60  
 DB 1 MNRGVPFRHLVLVQLALPPAATQGNKVVLGKGGDTVELTCTASOKKSIOPFMKNSNOIK 60  
 OY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
 DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
 OY 121 LVFGLTANSDTHLLQGOQLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGLTANSDTHLLQGOQLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 OY 181 TWCTCTVLONOKKVEFKIDIV 200  
 DB 181 TWCTCTVLONOKKVEFKIDIV 200

RESULT 69  
 AA59171  
 ID AA59171 standard; protein; 481 AA.

XX AC AA59171;  
 XX DT 14-MAR-2000 (first entry)  
 XX DE CD4-Ig fusion protein CD4Pmu.  
 XX KW HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;  
 XX KM secreted protein; SIV infection; medicament.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX PN CA1340741-C.  
 XX PD 14-SEP-1999.  
 XX PF 20-JAN-1989; 89CA-00588749.  
 XX PR 20-JAN-1989; 89CA-00588749.  
 XX PA (GEHO ) GEN HOSPITAL CORP.  
 XX PI Seed B;  
 XX WPI: 2000-063015/06.  
 XX DR N-PSDB; AA248204.

PT New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in  
 PT the treatment of HIV or simian immunodeficiency virus infections.  
 XX  
 PS Example 1; Page 54-60; 89pp; English.  
 XX

CC The invention provides a fusion gene encoding a fusion protein that  
 CC comprises an extracellular CD4 DNA sequence or its fragment which binds  
 CC to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA  
 CC sequence of an Ig heavy or light chain, where the DNA sequence encoding  
 CC the variable region has been replaced with the DNA sequence which encodes  
 CC extracellular CD4 or its gp120 binding fragment. The fusion protein is  
 CC capable of being secreted. The fusion proteins are useful for treating  
 CC HIV or SIV infections in animals, preferably humans. They are also useful  
 CC for producing medicaments which can be used for treating HIV or SIV  
 CC infections in humans. The present sequence represents the fusion protein  
 CC CD4Pmu where the CD4 is linked to human IgG1 at the Pst site upstream of  
 CC the CH2 region  
 XX  
 SQ Sequence 481 AA;

Query Match 77.7%; Score 1023; DB 3; Length 481;  
 Best Local Similarity 99.5%; Pred. No. 5.1e-63;  
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNRGVPFRHLVLVQLALPPAATQGNKVVLGKGGDTVELTCTASOKKSIOPFMKNSNOIK 60  
 DB 1 MNRGVPFRHLVLVQLALPPAATQGNKVVLGKGGDTVELTCTASOKKSIOPFMKNSNOIK 60  
 OY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
 DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
 OY 121 LVFGLTANSDTHLLQGOQLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGLTANSDTHLLQGOQLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
 OY 181 TWCTCTVLONOKKVEFKIDIV 200  
 DB 181 TWCTCTVLONOKKVEFKIDIV 200

RESULT 70  
 AAB00158  
 ID AAB00158 standard; protein; 507 AA.

XX AC AAB00158;  
 XX DT 08-FEB-2001 (first entry)  
 XX DE sCD4-sCPv(17b) HIV single chain antibody fusion protein.  
 XX KW Fusion protein; HIV; human immunodeficiency virus; antibody; Fv; AIDS;  
 XX KM acquired immune deficiency syndrome; neutralisation; infection;  
 XX KW gene therapy; CD4; gp120; glycoprotein; resistance; vaccination;  
 XX KM binding domain; single chain antibody; chimera; chimeric protein.  
 XX OS Human immunodeficiency virus.  
 XX OS Synthetic.  
 XX PN WO200055207-A1.  
 XX PD 21-SEP-2000.  
 XX PF 16-MAR-2000; 2000WO-US006946.  
 XX PR 16-MAR-1999; 99US-0124681P.  
 XX PA (USSH ) US NAT INST OF HEALTH.  
 XX PI Berger EA, Del Castillo CM;  
 XX WPI: 2000-638183/61.  
 XX DR N-PSDB; AAA54045.

XX Novel neutralizing bispecific fusion proteins effective in viral such as  
PT HIV neutralization, comprises two different binding domains, inducing-  
PT binding domain and induced-binding domain functionally linked by linker.  
XX  
PS Claim 39, Page 46-47; 55pp; English.

XX sCD4-SCFv(17b) is a neutralising bispecific fusion protein capable of  
CC binding to two sites of its target protein. The protein comprises a first  
CC binding domain capable of binding to an inducing site on the target  
CC protein, a second binding domain capable of forming neutralising complex  
CC with an induced epitope of the target protein and a linker connecting the  
CC binding domains. sCD4-SCFv(17b) comprises a soluble CD4 fragment  
CC (containing domains D1 and D2) fused to a single chain Fv portion of  
CC antibody 17b via a linker. sCD4-SCFv(17b), its variant, analogue or  
CC mimetic is used for inactivating gp120 protein of HIV, and for  
CC neutralising HIV. It is also used for blocking and preventing the binding  
CC of the viral or recombinant gp120 protein to soluble CD4 or lymphocyte  
CC CD4 and for inhibiting HIV replication. The chimeric proteins is  
CC therefore useful for treating HIV infection and also AIDS. It is are  
CC particularly useful in the prevention of infection during or immediately  
CC after HIV exposure (e.g., mother/infant transmission, post-exposure  
CC prophylaxis, and as a topical inhibitor) and for providing long term  
CC resistance to HIV infections and AIDS. Gene therapy is used to secrete  
CC the bispecific protein at mucosal surfaces, such as the vaginal, rectal  
CC or oral mucosa. The fusion proteins is highly potent, broadly cross-  
CC reactive with neutralising antibody with high in vivo activity and no FC-  
CC mediated undesirable targeting properties. When the fusion protein is  
CC substantially derived from human proteins, it has minimal immunogenicity  
CC and toxicity in humans which is of great value in prevention of infection  
CC during or immediately after HIV exposure  
XX  
SQ Sequence 507 AA;

Query Match 77.7%; Score 1023; DB 3; Length 507;  
Best Local Similarity 99.5%; Pred. No. 5.4e-63;  
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLTQALLPATQGNKVYLGKGGDTVELTCTASOKKSIOFHMKNSNOIK 60  
DB 1 MNRGVPFRHLVLTQALLPATQGNKVYLGKGGDTVELTCTASOKKSIOFHMKNSNOIK 60  
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120  
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120  
QY 121 LVFGLTANSDTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSDTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGKTLVSQLELDQSG 180  
QY 181 TWCTVVLQNOQKVEFKIDIV 200  
DB 181 TWCTVVLQNOQKVEFKIDIV 200

RESULT 71

AAR20152  
ID AAR20152 standard; protein; 519 AA.

XX AAR20152;

XX 25-MAR-2003 (revised)  
DT 31-MAR-1992 (first entry)  
XX

DE Human CD4 sequence encoded by PATY. 6.

XX Human immunodeficiency virus; HIV; gp 120; AIDS; ARC; glycoprotein;  
KW acquired immune deficiency syndrome; AIDS related complex;  
KM T helper lymphocytes.  
XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25  
/label= signal\_sequence

XX MO9118618-A.

XX 12-DEC-1991.

XX 25-MAY-1990; 90US-00529186.

XX 25-MAY-1990; 90US-00529186.

XX (BIOJ ) BIOGEN INC.

XX Fisher RA, Hession C, Burkly LC;

XX WPI; 1992-007200/01.

XX N-PSDB; AAQ20327.

XX New immuno-therapeutic human CD4 variants and derivs. - elicit AB  
PT production to HIV gp.120, useful in treating, preventing and diagnosing  
PT AIDS, ARC and HIV infections.

XX Disclosure; Fig 28; 179pp; English.

XX The sequence was deduced from the DNA sequence of subclone PATY.6, contg.  
CC DNA coding for the full-length human CD4. The clone was constructed from  
CC plasmids PBG178A and PBG378 (both in US8802940). The DNA can be used to  
CC express recombinant CD4 and analogues for use in diagnosis and treatment  
CC of diseases caused by infective agents whose primary targets are T4+  
CC lymphocytes. See also AAR20148-R20155 and AAR21078. (Updated on 25-MAR-  
CC 2003 to correct PA field.)  
XX

SQ Sequence 519 AA;

Query Match 77.7%; Score 1023; DB 2; Length 519;  
Best Local Similarity 99.5%; Pred. No. 5.5e-63;  
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLTQALLPATQGNKVYLGKGGDTVELTCTASOKKSIOFHMKNSNOIK 60  
DB 62 MNRGVPFRHLVLTQALLPATQGNKVYLGKGGDTVELTCTASOKKSIOFHMKNSNOIK 121  
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120  
DB 122 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 181  
QY 121 LVFGLTANSDTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGKTLVSQLELDQSG 180  
DB 182 LVFGLTANSDTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGKTLVSQLELDQSG 241  
QY 181 TWCTVVLQNOQKVEFKIDIV 200  
DB 242 TWCTVVLQNOQKVEFKIDIV 261

RESULT 72

AA551082  
ID AA551082 standard; protein; 616 AA.

XX AA551082;

XX 23-MAR-2000 (first entry)  
DT  
XX

DE Human fusion protein CD4Bgammal.

XX Fusion protein; human; CD4; IgG1; immunoglobulin; gp120;

XX anti-human immunodeficiency virus; CD4Bgammal.

XX Homo sapiens.

XX Synthetic.

XX US6004781-A.

PD 21-DEC-1999.  
XX  
PF 04-FEB-1994; 94US-00191708.  
XX  
PR 22-JAN-1988; 88US-00147351.  
PR 23-JAN-1989; 89US-00295956.  
PR 09-JUN-1992; 92US-0086781.  
PR 12-APR-1993; 93US-00057952.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI Seed B;  
XX  
DR WPI: 2000-085792/07.  
DR N-PSDB; AAZ44065.  
XX  
PT Fusion protein useful for the treatment of human immunodeficiency virus.  
XX  
PS Example 1; Col 59-70; 39pp; English.  
XX  
CC This invention describes a novel nucleic acid (I) encoding a fusion  
CC protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)  
CC and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light  
CC chain (III). The products of the invention have anti-human  
CC immunodeficiency virus (HIV) activity and are capable of binding to  
CC gp120. The fusion protein is useful for treating human immunodeficiency  
CC virus (HIV) or simian immunodeficiency virus (SIV). This sequence  
CC represents the fusion protein CD4Bgamma1 which is constructed from CD4  
CC linked to human IgG1 upstream of the hinge region  
XX  
SQ Sequence 616 AA;

Query Match 77.7%; Score 1023; DB 3; Length 616;  
Best Local Similarity 99.5%; Pred. No. 6.7e-63;  
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHKNNSQIK 60  
DB 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHKNNSQIK 60  
QY 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSDPHLLQGSQSLTLTLESPGSSPVQCRSPRGKNTQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSDPHLLQGSQSLTLTLESPGSSPVQCRSPRGKNTQGGKTLVSQLELDQSG 180  
QY 181 TWTCVTLOKQKVEFKIDIV 200  
DB 181 TWTCVTLOKQKVEFKIDIV 200

RESULT 73  
AAV59172  
ID AAV59172 standard; protein; 616 AA.  
XX  
AC AAV59172;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE CD4-Ig fusion protein CD4Bgamma1.  
XX  
KW HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;  
XX secreted protein; SIV infection; medicament.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN CA1340741-C.  
XX  
PD 14-SEP-1999.

PF 20-JAN-1989; 89CA-00588749.  
XX  
PR 20-JAN-1989; 89CA-00588749.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI Seed B;  
XX  
DR WPI: 2000-063015/06.  
DR N-PSDB; AAZ48205.  
XX  
PT New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in  
PT the treatment of HIV or simian immunodeficiency virus infections.  
XX  
PS Example 1; Page 61-68; 89pp; English.  
XX  
CC The invention provides a fusion gene encoding a fusion protein that  
CC comprises an extracellular CD4 DNA sequence or its fragment which binds  
CC to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA  
CC sequence of an Ig heavy or light chain, where the DNA sequence encoding  
CC the variable region has been replaced with the DNA sequence which encodes  
CC extracellular CD4 or its gp120 binding fragment. The fusion protein is  
CC capable of being secreted. The fusion proteins are useful for treating  
CC HIV or SIV infections in animals, preferably humans. They are also useful  
CC for producing medicaments which can be used for treating HIV or SIV  
CC infections in humans. The present sequence represents the fusion protein  
CC CD4Bgamma1 where the CD4 is linked to human IgG1 at the BamI site  
CC downstream from the hinge region  
XX  
SQ Sequence 616 AA;

Query Match 77.7%; Score 1023; DB 3; Length 616;  
Best Local Similarity 99.5%; Pred. No. 6.7e-63;  
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHKNNSQIK 60  
DB 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHKNNSQIK 60  
QY 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSDPHLLQGSQSLTLTLESPGSSPVQCRSPRGKNTQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSDPHLLQGSQSLTLTLESPGSSPVQCRSPRGKNTQGGKTLVSQLELDQSG 180  
QY 181 TWTCVTLOKQKVEFKIDIV 200  
DB 181 TWTCVTLOKQKVEFKIDIV 200

RESULT 74  
AAP93009  
ID AAP93009 standard; protein; 631 AA.  
XX  
AC AAP93009;  
XX  
DT 25-MAR-2003 (revised)  
DT 02-NOV-1992 (first entry)  
XX  
DE Genetic construct which encodes CD4 linked to human IgG1 at the Esp site  
DE upstream of the hinge region (fusion protein CD4B-gamma-1).  
XX  
KW Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;  
XX diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.  
XX  
OS Homo sapiens.  
XX  
PN EP325262-A.  
XX  
PD 26-JUL-1989.

```

PF 20-JAN-1989; 89EP-00100913.
XX
XX 22-JAN-1988; 88US-00147351.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B;
XX
XX WPI; 1989-214472/30.
XX N-PSDB; AAN90357.
XX
XX Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV
XX infections or detecting HIV or SIV in sample.
XX
XX Example; Table 2, Page 24-33; 68pp; English.
XX
XX The fusion protein genes of the invention pref. comprise cDNA sequences
XX which encode CD4 or a fragment which binds gp120 ligated to an expression
XX plasmid which encodes an antibody in which the variable region of the
XX gene has been deleted (see WO87-02671). The CD4 portion of the fusion
XX protein may comprise the complete CD4 sequence, the 370 AA extracellular
XX region and the membrane spanning domain, or the extracellular region. The
XX Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are
XX specifically claimed: fusion proteins CD4H-gamma-1, CD4Mmu, CD4Fmu, CD4E-
XX gamma1, and CD4Mmu (No. 67608), pCD4P-gamma (No. 67609) and pCD4E-gamma-1
XX (No. 67610). The plasmid containing (pCD4E-gamma-1) has been deposited in
XX E. coli (MC1061/P3) at the ATCC under accession number 67610. (Updated on
XX 25-MAR-2003 to correct PA field.)
XX
XX Sequence 631 AA;
XX
XX Query Match 77.7%; Score 1023; DB 1; Length 631;
XX Best Local Similarity 99.5%; Pred. No. 6,9e-63;
XX Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MNRGVPFRHLILVQLALIPATQGNKVVIGKGDVLTCTASQKKSIOFHMKNSNQIK 60
XX 1 MNRGVPFRHLILVQLALIPATQGNKVVIGKGDVLTCTASQKKSIOFHMKNSNQIK 60
XX
XX 61 ILNGQSFLLTKGPSKLNDRADSRSLMDQGNFPLIINKLIKIDSDTYICEVEDQKEEYOL 120
XX 61 ILNGQSFLLTKGPSKLNDRADSRSLMDQGNFPLIINKLIKIDSDTYICEVEDQKEEYOL 120
XX
XX 121 LVFGLTANSPTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
XX 121 LVFGLTANSPTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
XX
XX 181 TWTCTVLQONQKVEFFKIDIV 200
XX 181 TWTCTVLQONQKVEFFKIDIV 200
XX
XX Db 181 TWTCTVLQONQKVEFFKIDIV 200
XX
XX
XX RESULT 75
XX AAB19508
XX ID AAB19508 standard; protein; 631 AA.
XX
XX AC AAB19508;
XX
XX DT 09-JAN-2001 (first entry)
XX
XX DE CD4-IgG1 fusion protein CH4Bgammal.
XX
XX KM CD4; IgG1; human; CD4Bgammal; fusion protein; immunoglobulin; HIV; SIV;
XX gp120; therapy; diagnosis.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 1..395
XX FT /note="CD4 extracellular region"
XX FT Protein 400..631
XX /note="IgG1 heavy chain"
XX

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PN US6117656-A.
XX
XX 12-SEP-2000.
XX
XX 07-JUN-1995; 95US-00479353.
XX
XX 22-JAN-1988; 88US-00147351.
XX 23-JAN-1989; 89US-00299596.
XX 09-JUN-1992; 92US-00896781.
XX 12-APR-1993; 93US-00057952.
XX 04-FEB-1994; 94US-00191708.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B;
XX
XX WPI; 2000-586558/55.
XX N-PSDB; AAB50661.
XX
XX CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
XX SIV.
XX
XX Example 1; Col 29-42; 39pp; English.
XX
XX The present sequence is that of fusion protein CD4Bgammal comprising the
XX extracellular portion of CD4, which binds to HIV gp120, linked at its C-
XX terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA
XX encoding CD4 was linked to IgG1 DNA at the Esp site upstream of the hinge
XX region (see AAB50661). Fusion protein CD4Bgammal and a nucleic acid
XX encoding it are claimed. Also claimed are a vector comprising the nucleic
XX acid, and a method of producing the fusion protein in secreted form using
XX a transformed host cell. The fusion protein may further comprise a
XX therapeutic agent, radiolabel or NMR imaging agent. The fusion protein
XX can be administered to an animal (including humans) for treatment of HIV
XX or SIV infection, and can also be used in assays for HIV or SIV, imaging
XX and tissue stains. IgG1 fusion proteins such as CD4Bgammal provide both
XX complement-mediated and cell-mediated immunity
XX
XX Sequence 631 AA;
XX
XX Query Match 77.7%; Score 1023; DB 3; Length 631;
XX Best Local Similarity 99.5%; Pred. No. 6,9e-63;
XX Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MNRGVPFRHLILVQLALIPATQGNKVVIGKGDVLTCTASQKKSIOFHMKNSNQIK 60
XX 1 MNRGVPFRHLILVQLALIPATQGNKVVIGKGDVLTCTASQKKSIOFHMKNSNQIK 60
XX
XX 61 ILNGQSFLLTKGPSKLNDRADSRSLMDQGNFPLIINKLIKIDSDTYICEVEDQKEEYOL 120
XX 61 ILNGQSFLLTKGPSKLNDRADSRSLMDQGNFPLIINKLIKIDSDTYICEVEDQKEEYOL 120
XX
XX 121 LVFGLTANSPTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
XX 121 LVFGLTANSPTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
XX
XX 181 TWTCTVLQONQKVEFFKIDIV 200
XX 181 TWTCTVLQONQKVEFFKIDIV 200
XX
XX Db 181 TWTCTVLQONQKVEFFKIDIV 200
XX
XX
XX RESULT 76
XX AAY51079
XX ID AAY51079 standard; protein; 631 AA.
XX
XX AC AAY51079;
XX
XX DT 23-MAR-2000 (first entry)
XX
XX DE Human fusion protein CD4Bgammal.
XX
XX KM Fusion protein; human; CD4; IgG1; immunoglobulin; gp120;
XX anti-human immunodeficiency virus; CD4Bgammal.
XX

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```
XX Homo sapiens.
OS Synthetic.
XX US604781-A.
XX 21-DEC-1999.
XX 04-FEB-1994; 94US-00191708.
XX 22-JAN-1988; 88US-00147351.
XX 23-JAN-1989; 89US-00295956.
XX 09-JUN-1992; 92US-0086781.
XX 12-APR-1993; 93US-00057952.
XX (GENO ) GEN HOSPITAL CORP.
XX Seed B;
XX WPI: 2000-085792/07.
XX N-PSDB; AAZ44062.
XX Fusion protein useful for the treatment of human immunodeficiency virus.
XX Example 1; Col 29-42; 39pp; English.
XX This invention describes a novel nucleic acid (I) encoding a fusion
XX protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)
XX and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light
XX chain (III). The products of the invention have anti-human
XX immunodeficiency virus (HIV) activity and are capable of binding to
XX gp120. The fusion protein is useful for treating human immunodeficiency
XX virus (HIV) or simian immunodeficiency virus (SIV). This sequence
XX represents the fusion protein CD4Bgamma1 which is constructed from CD4
XX linked to human IgG1 upstream of the hinge region
XX
SQ Sequence 631 AA;
Query Match 77.7%; Score 1023; DB 3; Length 631;
Best Local Similarity 99.5%; Pred. No. 6.9e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNRGVPFRHLILVQLALPAAATQGNKVVLGKGGDVELTCTASOKKSIOFHMKNNOIK 60
DB 1 MNRGVPFRHLILVQLALPAAATQGNKVVLGKGGDVELTCTASOKKSIOFHMKNNOIK 60
QY 61 ILGNQGSFLLTKGSPKLNDRADSRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLLTKGSPKLNDRADSRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDPTHLLOQGSLLTLTLESPGSSPSVQCRSPRKNIOGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDPTHLLOQGSLLTLTLESPGSSPSVQCRSPRKNIOGKTLVSQLELDQSG 180
QY 181 TWTCVLONOKKVEFKIDIV 200
DB 181 TWTCVLONOKKVEFKIDIV 200
RESULT 77
AAV59169
ID AAV59169 standard; protein; 631 AA.
XX
XX AAV59169;
XX 14-MAR-2000 (first entry)
XX CD4-Ig fusion protein CD4Bgamma1.
XX HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;
XX secreted protein; SIV infection; medication.
XX Synthetic.
```

```
OS Homo sapiens.
XX CA1340741-C.
XX 14-SEP-1999.
XX 20-JAN-1989; 89CA-00588749.
XX 20-JAN-1989; 89CA-00588749.
XX 20-JAN-1989; 89CA-00588749.
XX (GENO ) GEN HOSPITAL CORP.
XX Seed B;
XX WPI: 2000-063015/06.
XX N-PSDB; AAZ48202.
XX New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in
XX the treatment of HIV or simian immunodeficiency virus infections.
XX Example 1; Page 37-46; 89pp; English.
XX The invention provides a fusion gene encoding a fusion protein that
XX comprises an extracellular CD4 DNA sequence or its fragment which binds
XX to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA
XX sequence of an Ig heavy or light chain, where the DNA sequence encoding
XX the variable region has been replaced with the DNA sequence which encodes
XX extracellular CD4 or its gp120 binding fragment. The fusion protein is
XX capable of being secreted. The fusion proteins are useful for treating
XX HIV or SIV infections in animals, preferably humans. They are also useful
XX for producing medicaments which can be used for treating HIV or SIV
XX infections in humans. The present sequence represents the fusion protein
XX CD4Bgamma1 where the CD4 is linked to human IgG1 at the Bsp site upstream
XX of the hinge region
XX
SQ Sequence 631 AA;
Query Match 77.7%; Score 1023; DB 3; Length 631;
Best Local Similarity 99.5%; Pred. No. 6.9e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNRGVPFRHLILVQLALPAAATQGNKVVLGKGGDVELTCTASOKKSIOFHMKNNOIK 60
DB 1 MNRGVPFRHLILVQLALPAAATQGNKVVLGKGGDVELTCTASOKKSIOFHMKNNOIK 60
QY 61 ILGNQGSFLLTKGSPKLNDRADSRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLLTKGSPKLNDRADSRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDPTHLLOQGSLLTLTLESPGSSPSVQCRSPRKNIOGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDPTHLLOQGSLLTLTLESPGSSPSVQCRSPRKNIOGKTLVSQLELDQSG 180
QY 181 TWTCVLONOKKVEFKIDIV 200
DB 181 TWTCVLONOKKVEFKIDIV 200
RESULT 78
AAP93008
ID AAP93008 standard; protein; 729 AA.
XX
XX AAP93008;
XX 25-MAR-2003 (revised)
XX 02-NOV-1992 (first entry)
XX Genetic construct which encodes CD4 linked to human IgG1 at the Hind3
XX site upstream of the CH1 region (fusion protein CD4H-gamma-1).
XX Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;
XX diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.
XX
```

```

OS Homo sapiens.
XX
XX EP325262-A.
XX
XX 26-JUL-1989.
XX
XX 20-JAN-1989; 89EP-00100913.
XX
XX 22-JAN-1988; 88US-00147351.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B;
XX
XX WPI; 1989-214472/30.
XX
XX N-PSDB; AAN90356.
XX
XX Immunoglobulin-CD4 fusion proteins - used for creating HIV or SIV
XX
XX infections or detecting HIV or SIV in sample.
XX
XX Example; Table 1, Page 12-23; 68pp; English.
XX
XX The fusion protein genes of the invention pref. comprise cDNA sequences
XX
XX which encode CD4 or a fragment which binds gp120 ligated to an expression
XX
XX plasmid which encodes an antibody in which the variable region of the
XX
XX gene has been deleted (see WO87-02671). The CD4 portion of the fusion
XX
XX protein may comprise the complete CD4 sequence, the 370 AA extracellular
XX
XX region and the membrane spanning domain, or the extracellular region. The
XX
XX Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are
XX
XX specifically claimed: fusion proteins CD4H-gamma-1, CD4Mu, CD4Fmu, CD4E-
XX
XX gamma1, and CD4Fmu (No. 67608), pCD4P-gamma (No. 67609) and pCD4E-gamma-1
XX
XX (No. 67610). The plasmid containing (pCD4H-gamma-1) has been deposited in
XX
XX E. coli (MC1061/P3) at the ATCC under accession number 67611. (Updated on
XX
XX 25-MAR-2003 to correct PA field.)
XX
XX Sequence 729 AA;
XX
XX Query Match 77.7%; Score 1023; DB 1; Length 729;
XX
XX Best Local Similarity 99.5%; Pred. No. 8.1e-63;
XX
XX Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
XX
XX 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
XX
XX 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVL 120
XX
XX 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVL 120
XX
XX 121 LVFGLTANSDTHLLQGQSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLISVQLLEIDSG 180
XX
XX 121 LVFGLTANSDTHLLQGQSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLISVQLLEIDSG 180
XX
XX 181 TWICTVLOKQKVEFKIDIV 200
XX
XX 181 TWICTVLOKQKVEFKIDIV 200
XX
XX Db
XX
XX RESULT 79
XX
XX AAB19507 standard; protein; 729 AA.
XX
XX AAB19507;
XX
XX 09-JAN-2001 (first entry)
XX
XX CD4-IgG1 fusion protein CH4Hgamma1.
XX
XX CD4; IgG1; human; CD4Hgamma1; fusion protein; immunoglobulin; HIV; SIV;
XX
XX gp120; therapy; diagnosis.
XX
XX Homo sapiens.
XX

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FH Key Location/Qualifiers
FT Protein 1..395
FT /note= "CD4 extracellular region"
FT Protein 400..729
FT /note= "IgG1 heavy chain"
XX
XX US6117656-A.
XX
XX 12-SEP-2000.
XX
XX 07-JUN-1995; 95US-00479353.
XX
XX 22-JAN-1988; 88US-00147351.
XX
XX 23-JAN-1989; 89US-00293596.
XX
XX 09-JUN-1989; 89US-00896781.
XX
XX 12-APR-1993; 93US-00057952.
XX
XX 04-FEB-1994; 94US-00191708.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B;
XX
XX WPI; 2000-586558/55.
XX
XX N-PSDB; AAA50660.
XX
XX CD4-Immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
XX
XX SIV.
XX
XX Example 1; Col 13-30; 39pp; English.
XX
XX The present sequence is that of fusion protein CD4Hgamma1 comprising the
XX
XX extracellular portion of CD4, which binds to HIV gp120, linked at its C-
XX
XX terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA
XX
XX encoding CD4 was linked to IgG1 DNA at the HindIII site upstream of the CH1
XX
XX region (see AAA50660). Fusion protein CD4Hgamma1 and a nucleic acid
XX
XX encoding it are claimed. Also claimed are a vector comprising the nucleic
XX
XX acid, and a method of producing the fusion protein in secreted form using
XX
XX a transformed host cell. The fusion protein may further comprise a
XX
XX therapeutic agent, radiolabel or NMR imaging agent. The fusion protein
XX
XX can be administered to an animal (including humans) for treatment of HIV
XX
XX or SIV infection, and can also be used in assays for HIV or SIV, imaging
XX
XX and tissue stains. IgG1 fusion proteins such as CD4Hgamma1 provide both
XX
XX complement-mediated and cell-mediated immunity
XX
XX Sequence 729 AA;
XX
XX Query Match 77.7%; Score 1023; DB 3; Length 729;
XX
XX Best Local Similarity 99.5%; Pred. No. 8.1e-63;
XX
XX Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
XX
XX 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
XX
XX 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVL 120
XX
XX 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVL 120
XX
XX 121 LVFGLTANSDTHLLQGQSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLISVQLLEIDSG 180
XX
XX 121 LVFGLTANSDTHLLQGQSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLISVQLLEIDSG 180
XX
XX 181 TWICTVLOKQKVEFKIDIV 200
XX
XX 181 TWICTVLOKQKVEFKIDIV 200
XX
XX Db
XX
XX RESULT 80
XX
XX AAY51078 standard; protein; 729 AA.
XX
XX AAY51078;
XX

```

```
DT 23-MAR-2000 (first entry)
XX
DE Human fusion protein CD4H-1.
XX
KW Fusion protein; human; CD4; IgG1; immunoglobulin; gp120;
KM anti-human immunodeficiency virus; CD4H-1.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6004781-A.
XX
PD 21-DEC-1999.
XX
PF 04-FEB-1994; 94US-00191708.
XX
PR 22-JAN-1988; 88US-00147351.
PR 23-JAN-1989; 89US-00295956.
PR 09-JUN-1992; 92US-00896781.
PR 12-APR-1993; 93US-00057952.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI Seed B;
XX
DR WPI; 2000-085792/07.
DR N-PSDB; AAZ44061.
XX
PT Fusion protein useful for the treatment of human immunodeficiency virus.
XX
PS Example 1; Col 15-30; 39pp; English.
XX
CC This invention describes a novel nucleic acid (I) encoding a fusion
CC protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)
CC and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light
CC chain (III). The products of the invention have anti-human
CC immunodeficiency virus (HIV) activity and are capable of binding to
CC gp120. The fusion protein is useful for treating human immunodeficiency
CC virus (HIV) or simian immunodeficiency virus (SIV). This sequence
CC represents the fusion protein CD4H-1 which is constructed from CD4 linked
CC to human IgG1 upstream of the CH1 region
XX
SQ Sequence 729 AA;

Query Match 77.7%; Score 1023; DB 3; Length 729;
Best Local Similarity 99.5%; Pred. No. 8.1e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPRRHLLVQLALPPAATQGNKVLGKGGDTVELTCTASOKKSIQFHKNSNQIK 60
DB 1 MNRGVPRRHLLVQLALPPAATQGNKVLGKGGDTVELTCTASOKKSIQFHKNSNQIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLWDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLWDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLTSSQLLELDGSG 180
DB 121 LVFGLTANSDTHLLQGSQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLTSSQLLELDGSG 180
QY 181 TWICTVLONOKVEFKIDIV 200
DB 181 TWICTVLONOKVEFKIDIV 200

RESULT 81
AAVS9168
ID AAVS9168 standard; protein; 729 AA.
XX
AC AAVS9168;
XX
DT 14-MAR-2000 (first entry)
XX
```

```
DE CD4-Ig fusion protein CD4Hgamma1.
XX
KM HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;
KM secreted protein; SIV infection; medicament.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN CA1340741-C.
XX
PD 14-SEP-1999.
XX
PF 20-JAN-1989; 89CA-00588749.
XX
PR 20-JAN-1989; 89CA-00588749.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI Seed B;
XX
DR WPI; 2000-063015/06.
DR N-PSDB; AAZ48201.
XX
PT New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in
PT the treatment of HIV or simian immunodeficiency virus infections.
XX
PS Example 1; Page 25-36; 89pp; English.
XX
CC The invention provides a fusion gene encoding a fusion protein that
CC comprises an extracellular CD4 DNA sequence or its fragment which binds
CC to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA
CC sequence of an Ig heavy or light chain, where the DNA sequence encoding
CC the variable region has been replaced with the DNA sequence which encodes
CC extracellular CD4 or its gp120 binding fragment. The fusion protein is
CC capable of being secreted. The fusion proteins are useful for treating
CC HIV or SIV infections in animals, preferably humans. They are also useful
CC for producing medicaments which can be used for treating HIV or SIV
CC infections in humans. The present sequence represents the fusion protein
CC CD4Hgamma1 where the CD4 is linked to human IgG1 at the Hind3 site
CC upstream of the CH1 region
XX
SQ Sequence 729 AA;

Query Match 77.7%; Score 1023; DB 3; Length 729;
Best Local Similarity 99.5%; Pred. No. 8.1e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPRRHLLVQLALPPAATQGNKVLGKGGDTVELTCTASOKKSIQFHKNSNQIK 60
DB 1 MNRGVPRRHLLVQLALPPAATQGNKVLGKGGDTVELTCTASOKKSIQFHKNSNQIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLWDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLWDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLTSSQLLELDGSG 180
DB 121 LVFGLTANSDTHLLQGSQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLTSSQLLELDGSG 180
QY 181 TWICTVLONOKVEFKIDIV 200
DB 181 TWICTVLONOKVEFKIDIV 200

RESULT 82
AAR26530
ID AAR26530 standard; protein; 435 AA.
XX
AC AAR26530;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1993 (first entry)
XX
```

DE Sequence of one chain of a CD4-gamma 1 chimeric heavy chain homodimer.  
XX  
XX CD4-gamma 1 chimeric heavy chain homodimer; expression vector; HIV;  
XM therapy; diagnostic agent; inhibition.  
XX  
OS Synthetic.  
XX  
FH Key  
FT Region 1. 204  
FT /label= CD4  
FT /note="1. 25 = prerregion"  
FT /label= hinge  
FT 205. 219  
FT Region /label= hinge  
FT 220. 329  
FT Region /label= CH2  
FT 330. 436  
FT Region /label= CH3  
XX  
XX WO9213559-A1.  
XX  
XX 20-AUG-1992.  
XX  
XX 10-FEB-1992; 92WO-US001152.  
XX  
XX 08-FEB-1991; 91US-00654205.  
XX  
XX (PROG-) PROGENICS PHARM INC.  
XX  
XX Beaudry GA, Maddon PJ;  
XX  
XX WPI; 1992-299758/36.  
XX  
XX N-PSDB; AAQ27830.  
XX  
XX CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector -  
PT for preventing and creating HIV infection useful as a diagnostic agent.  
XX  
XX Example; Fig 3; 89pp; English.  
XX  
XX Human CD4 cDNA was excised from pSPET4 and cloned into M13mp18. The 2 kb  
CC PetI/PstI fragment from pBR lambda 1 contg. the human lambda 1 heavy  
CC chain gene (contg. the hinge, CH2 and CH3 exons) was isolated and cloned  
CC into the BamI-treated M13mp18/CD4 vector. To obtain a CD4-lambda 1  
CC chimeric heavy chain gene, oligonucleotide-mediated site-directed  
CC mutagenesis was performed to juxtapose the CD4 and lambda 1 heavy chain  
CC DNA sequences, ligating the CD4 sequence in frame to the hinge exon. The  
CC DNA was then cloned into pCDNA-1 to produce CD4-IgG1-pCDNA1 (ATCC 40951).  
CC (Updated on 25-MAR-2003 to correct FN field.)  
XX  
XX Sequence 435 AA;  
SQ  
Query Match 77.6%; Score 1021.5; DB 2; Length 435;  
Best Local Similarity 86.8%; Pred. No. 5.8e-63;  
Matches 204; Conservative 1; Mismatches 21; Indels 9; Gaps 1;  
QY 2 NRGVPRHLILVQLALLPAATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNOIKI 61  
DB 1 NRGVPRHLILVQLALLPAATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNOIKI 60  
QY 62 LSGNGSFLTGKPSKLNDRADSRSLMDQGNPPLIIKMLKTEDSDTYICEVEDQKEEVQL 121  
DB 61 LSGNGSFLTGKPSKLNDRADSRSLMDQGNPPLIIKMLKTEDSDTYICEVEDQKEEVQL 120  
QY 122 VFGLTANSDTHLLQGGSLTTLTSSPGSSPSVOCRSRPGKNIQGGKTLVSQLELDQSG 181  
DB 121 VFGLTANSDTHLLQGGSLTTLTSSPGSSPSVOCRSRPGKNIQGGKTLVSQLELDQSG 180  
QY 182 WTCITVLQNKQKVEFKIDIV-----PRASALPAAPTGSALPDPTASALPDP 227  
DB 181 WTCITVLQNKQKVEFKIDIVLAFEPKSCDKTHCPCPAPPELLGGSVFLFPKP 235  
RESULT 83  
ADE65841

ID ADE65841 standard; protein; 458 AA.  
XX  
XX ADE65841;  
AC  
XX 29-JAN-2004 (first entry)  
DT  
XX Human CD4 receptor.  
DE  
XX Human; CD4 receptor; receptor; protein-protein interaction;  
XM protein array; PDZ domain; drug target screening.  
XX  
OS Homo sapiens.  
XX  
XX US2003170723-A1.  
XX  
XX 11-SEP-2003.  
PD  
XX  
XX 06-MAR-2002; 2002US-00092138.  
PF  
XX  
XX 06-MAR-2002; 2002US-00092138.  
PR  
XX  
XX (SATO/) SATO T.  
PA  
XX  
XX Sato T;  
PI  
XX  
XX WPI; 2003-852032/79.  
DR  
XX  
XX  
PT Preparing a protein array useful for screening drug targets comprises  
PT depositing an array of a first protein on substrate, and applying a  
PT second protein comprising an amino acid sequence that binds to a domain  
PT of the first protein.  
XX  
XX  
XX Disclosure; SEQ ID NO 25; 60pp; English.  
PS  
XX  
XX The invention relates to a method for preparing a protein array based on  
CC protein-protein interaction, by depositing an array of a first protein  
CC comprising a PDZ domain on a substrate, and applying a second protein  
CC comprising an amino acid sequence that binds to the PDZ domain of the  
CC first protein. The method is useful for preparing protein arrays based on  
CC biochemical protein-protein interactions. Arrays produced by this method  
CC are useful for screening drug targets. This sequence represents the human  
CC CD4 receptor, used in the method of the invention.  
XX  
XX Sequence 458 AA;  
SQ  
Query Match 77.5%; Score 1021; DB 7; Length 458;  
Best Local Similarity 99.0%; Pred. No. 6.7e-63;  
Matches 198; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 NRGVPRHLILVQLALLPAATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNOIKI 60  
DB 1 NRGVPRHLILVQLALLPAATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNOIKI 60  
QY 61 ILSNGSFLTGKPSKLNDRADSRSLMDQGNPPLIIKMLKTEDSDTYICEVEDQKEEVQL 120  
DB 61 ILSNGSFLTGKPSKLNDRADSRSLMDQGNPPLIIKMLKTEDSDTYICEVEDQKEEVQL 120  
QY 121 LVFGLTANSDTHLLQGGSLTTLTSSPGSSPSVOCRSRPGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSDTHLLQGGSLTTLTSSPGSSPSVOCRSRPGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCTVLQNKQKVEFKIDIV 200  
DB 181 TWTCTVLQNKQKVEFKIDIV 200  
RESULT 84  
AAP93012  
ID AAP93012 standard; protein; 614 AA.  
XX  
XX AAP93012;  
AC  
XX  
XX 25-MAR-2003 (revised)  
DT

DT 03-AUG-1992 (first entry)  
 XX Genetic construct which encodes CD4 linked to human IgG1 at the BamI site  
 DE downstream from the hinge region (fusion protein CD4B1ambda1).  
 DE  
 KW Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;  
 KW diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPJ25262-A.  
 XX  
 PD 26-JUL-1989.  
 XX  
 PF 20-JAN-1989; 89EP-00100913.  
 XX  
 PR 22-JAN-1988; 88US-00147351.  
 XX  
 PA (GENO ) GEN HOSPITAL CORP.  
 XX  
 PI Seed B;  
 XX  
 DR WPI; 1989-214472/30.  
 DR N-PSDB; AAN90360.  
 XX  
 PT Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV  
 PT infections or detecting HIV or SIV in sample.  
 XX  
 PS Example; Table 5, Page 48-55; 68pp; English.  
 XX  
 CC The fusion protein genes of the invention pref. comprises cDNA sequences  
 CC which encode CD4 or a fragment which binds gp120 ligated to an expression  
 CC plasmid which encodes an antibody in which the variable region of the  
 CC gene has been deleted (see WO87-02671). The CD4 portion of the fusion  
 CC protein may comprise the complete CD4 sequence, the 370 AA extracellular  
 CC region and the membrane spanning domain, or the extracellular region. The  
 CC Ig heavy chain is pref. from IGM, IGK1 or IGK3. The following are  
 CC specifically claimed: fusion proteins CD4H1ambda1, CD4Mmu, CD4Pmu,  
 CC CD4E1ambda1, and CD4Mmu (No. 67608), pCD4H1ambda1 (No. 67609) and  
 CC pCD4E1ambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)  
 CC  
 XX  
 SQ Sequence 614 AA;  
 XX

Query Match 77.3%; Score 1018; DB 1; Length 614;  
 Best Local Similarity 99.0%; Pred. No. 1.5e-62;  
 Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLLVQLALPAAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60  
 DB 1 MNRGVPRHLLLVQLALPAAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60  
 QY 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICVEVDQKEEVOL 120  
 DB 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICVEVDQKEEVOL 120  
 QY 121 LVEGLTANSDPHLLQGSGLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDGSG 180  
 DB 121 LVEGLTANSDPHLLQGSGLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDGSG 180  
 QY 181 TWTCTVLQNGKKEVEFKIDIV 200  
 DB 181 TWTCTVLQNGKKEVEFKIDIV 200

RESULT 85  
 AAB93011  
 ID AAB93011 standard; protein; 481 AA.  
 XX  
 AC AAB93011;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 03-AUG-1992 (first entry)  
 XX

DE Genetic construct which encodes CD4 linked to human IGM at the PstI site  
 DE upstream of the CH2 region (fusion protein CD4Pmu).  
 DE  
 KW Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;  
 KW diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EPJ25262-A.  
 XX  
 PD 26-JUL-1989.  
 XX  
 PF 20-JAN-1989; 89EP-00100913.  
 XX  
 PR 22-JAN-1988; 88US-00147351.  
 XX  
 PA (GENO ) GEN HOSPITAL CORP.  
 XX  
 PI Seed B;  
 XX  
 DR WPI; 1989-214472/30.  
 DR N-PSDB; AAN90359.  
 XX  
 PT Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV  
 PT infections or detecting HIV or SIV in sample.  
 XX  
 PS Example; Table 4, Page 41-47; 68pp; English.  
 XX  
 CC The fusion protein genes of the invention pref. comprises cDNA sequences  
 CC which encode CD4 or a fragment which binds gp120 ligated to an expression  
 CC plasmid which encodes an antibody in which the variable region of the  
 CC gene has been deleted (see WO87-02671). The CD4 portion of the fusion  
 CC protein may comprise the complete CD4 sequence, the 370 AA extracellular  
 CC region and the membrane spanning domain, or the extracellular region. The  
 CC Ig heavy chain is pref. from IGM, IGK1 or IGK3. The following are  
 CC specifically claimed: fusion proteins CD4H1ambda1, CD4Mmu, CD4Pmu,  
 CC CD4E1ambda1, and CD4Mmu (No. 67608), pCD4H1ambda1 (No. 67609) and  
 CC pCD4E1ambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)  
 CC  
 XX  
 SQ Sequence 481 AA;  
 XX

Query Match 77.1%; Score 1015; DB 1; Length 481;  
 Best Local Similarity 99.0%; Pred. No. 1.8e-62;  
 Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLLVQLALPAAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60  
 DB 1 MNRGVPRHLLLVQLALPAAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60  
 QY 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICVEVDQKEEVOL 120  
 DB 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICVEVDQKEEVOL 120  
 QY 121 LVEGLTANSDPHLLQGSGLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDGSG 180  
 DB 121 LVEGLTANSDPHLLQGSGLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDGSG 180  
 QY 181 TWTCTVLQNGKKEVEFKIDIV 200  
 DB 181 TWTCTVLQNGKKEVEFKIDIV 200

RESULT 86  
 AAB07768  
 ID AAB07768 standard; protein; 394 AA.  
 XX  
 AC AAB07768;  
 XX  
 DT 07-NOV-2000 (first entry)  
 DE The soluble extracellular domain of the T4 glycoprotein.  
 XX Human; T4 glycoprotein; human immunodeficiency virus; HIV;  
 XX

KM envelope glycoprotein; AIDS; virus binding.  
 XX OS Homo sapiens.  
 XX PN US6093539-A.  
 XX PD 25-JUL-2000.  
 XX PF 06-JUN-1995; 95US-00466368.  
 XX PR 21-AUG-1986; 86US-00898587.  
 XX PR 11-JUN-1991; 91US-00713564.  
 XX PR 06-JUL-1992; 92US-00909021.  
 XX PR 12-DEC-1994; 94US-00354452.  
 XX PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX PI Madden PJ, Chess L, Axel R, Weiss R, McDougal JS, Littman DR;  
 XX WPI; 2000-505203/45.  
 XX DR N-PSDB; AAA59351.  
 XX PT New isolated nucleic acid encoding a human T cell surface protein and the  
 XX PT soluble surface T4 glycoprotein that it encodes, useful as prophylaxis  
 XX PT for treating a subject infected with human acquired immune deficiency  
 XX PT syndrome virus.  
 XX PS Disclosure; Col 11-14; 69pp; English.  
 XX CC The present sequence represents an aqueous-soluble polypeptide comprising  
 XX CC a portion of a human T4 glycoprotein. The portion specifically forms a  
 XX CC complex with a human immunodeficiency virus (HIV) envelope glycoprotein.  
 XX CC The DNA is useful for producing the soluble surface T4 glycoprotein. The  
 XX CC soluble surface T4 glycoprotein is useful as a therapeutic agent, i.e. as  
 XX CC prophylaxis for treating a subject infected with an HIV virus. Thus, the  
 XX CC soluble T4 glycoprotein is useful for treating human AIDS. The soluble T4  
 XX CC glycoprotein is also useful in diagnostic or screening assays, e.g. for  
 XX CC screening inhibitors of virus binding, or for detecting and quantitating  
 XX CC T4, T4+ cells and antibodies to T4, which are of diagnostic value for  
 XX CC AIDS  
 XX SQ Sequence 394 AA;  
 XX  
 Query Match 76.8%; Score 1012; DB 3; Length 394;  
 Best Local Similarity 98.5%; Pred. No. 2,4e-62;  
 Matches 197; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MNRGVFRRHLLVQLALPAATQGNKVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60  
 DB 1 MNRGVFRRHLLVQLALPAATQGNKVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60  
 QY 61 ILNQGSSFLTKGSPSKINDRADSRSLMDGNPPLIINKIKIDSDTYICEVEDQKEVOL 120  
 DB 61 ILNQGSSFLTKGSPSKINDRADSRSLMDGNPPLIINKIKIDSDTYICEVEDQKEVOL 120  
 QY 121 LVFGLTANSDTHLLOQSLTLTLSPGSSPSVQCRSPRKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGLTANSDTHLLOQSLTLTLSPGSSPSVQCRSPRKNIQGGKTLVSQLELDQSG 180  
 QY 181 TWTCVTLQONQKVEFKIDIV 200  
 DB 181 TWTCVTLQONQKVEFKIDIV 200  
 RESULT 87  
 AAR06373 standard; protein; 458 AA.  
 ID AAR06373  
 XX AAR06373;  
 AC XX  
 DT 31-OCT-2002 (revised)  
 DT 20-DEC-1990 (first entry)  
 XX

DE T4 encoded by plasmid p170-2.  
 XX  
 XX KW plasmid p170-2; soluble T4 protein; AIDS; ARC; HIV.  
 XX OS Synthetic.  
 XX FH Key  
 XX FH Peptide  
 XX FT 1..23  
 XX FT /label= hydrophobic/secretory signal  
 XX FT 24..117  
 XX FT /label= extracellular  
 XX FT /note= "homology to V-regions"  
 XX FT 118..132  
 XX FT /label= extracellular  
 XX FT /note= "homology to J-regions"  
 XX FT 133..397  
 XX FT /label= extracellular  
 XX FT /note= "glycosylated region"  
 XX FT 398..418  
 XX FT /label= transmembrane sequence  
 XX FT /note= "hydrophobic"  
 XX FT 419..458  
 XX FT /label= intracytoplasmic  
 XX FT /note= "very hydrophilic"  
 XX PN WO9008198-A.  
 XX PD 26-JUL-1990.  
 XX PF 18-JAN-1989; 89US-00300096.  
 XX PR 18-JAN-1989; 89US-00300096.  
 XX PA (HARD ) HARVARD COLLEGE.  
 XX PI Letvin NA;  
 XX DR WPI; 1990-254040/33.  
 XX DR N-PSDB; AAQ05607.  
 XX PT Treating or preventing AIDS, ARC or HIV infection - by administering an  
 XX PT immunologically effective amt. of soluble T4 protein.  
 XX PS Disclosure; Fig 1; 121pp; English.  
 XX CC Soluble T4 can be produced by truncating the CDS to remove the  
 XX CC transmembrane and cytoplasmic domains. The soluble forms may be modified  
 XX CC to increase their immunogenicity by addition of an adjuvant such as  
 XX CC incomplete Freund's adjuvant. The T4 interferes with HIV/T4 interaction  
 XX CC and elicits anti-soluble T4 antibody production. Soluble T4 proteins  
 XX CC include the following polypeptide fragments: amino acids 1-385, 24-385,  
 XX CC Met-24-385, 24-397, 1-400 and Met-24-400. See also AAQ05608. (Updated on  
 XX CC 31-OCT-2002 to add missing OS field.)  
 XX SQ Sequence 458 AA;  
 XX  
 Query Match 76.6%; Score 1009; DB 2; Length 458;  
 Best Local Similarity 99.0%; Pred. No. 4.5e-62;  
 Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MNRGVFRRHLLVQLALPAATQGNKVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60  
 DB 1 MNRGVFRRHLLVQLALPAATQGNKVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60  
 QY 61 ILNQGSSFLTKGSPSKINDRADSRSLMDGNPPLIINKIKIDSDTYICEVEDQKEVOL 120  
 DB 61 ILNQGSSFLTKGSPSKINDRADSRSLMDGNPPLIINKIKIDSDTYICEVEDQKEVOL 120  
 QY 121 LVFGLTANSDTHLLOQSLTLTLSPGSSPSVQCRSPRKNIQGGKTLVSQLELDQSG 180  
 DB 121 LVFGLTANSDTHLLOQSLTLTLSPGSSPSVQCRSPRKNIQGGKTLVSQLELDQSG 180  
 QY 181 TWTCVTLQONQKVEFKIDIV 200

Db 181 TWICTVLIQNGKVKVEFKIDIV 200

## RESULT 88

AAP94703  
ID AAP94703 standard; protein; 524 AA.

XX AAP94703;

XX 25-MAR-2003 (revised)

DT 22-MAR-1991 (first entry)

XX Sequence encoded by T4 lymphocyte cDNA obtained from PBL clone lambda-203

DE -4.

XX HIV; soluble T4; immunotherapeutic; prophylactic; diagnostic; AIDS; ARC.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 67 /note= "AA DESIGNATED NUMBER -23"

FT Misc-difference 90 /note= "AA DESIGNATED NUMBER 1"

FT Misc-difference 92 /note= "MATURE N-TERMINUS"

FT MO8901940-A.

PN 09-MAR-1989.

PD 01-SEP-1988; 88WO-US002940.

XX 04-SEP-1987; 87US-00094322.

XX 07-JAN-1988; 88US-00141649.

XX (BIOJ ) BIOGEN INC.

PI Fisher RA, Gilbert W, Sato VL, Flavell RA, Maraganore JM;

XX WPI; 1989-085519/11.

DR N-PSDB; AAN90642.

XX DNA sequences coding for soluble T4-like polypeptide(s) - used in

PT immuno:therapeutic and immunosuppressive compns. and for preventing,

PT creating or detecting AIDS.

XX Disclosure; Fig 3; 207pp; English.

XX The polypeptides encoded are useful in immunotherapeutic, prophylactic

CC and diagnostic compns. They can be used to purify HIV from a sample. The

CC soluble T4 protein-based compns. are useful in treating immunodeficient

CC patients suffering from diseases caused by agents whose primary targets

CC are T4+ lymphocytes. They can be used for preventing, treating or

CC detecting AIDS, ARC and HIV infection. (Updated on 25-MAR-2003 to correct

CC PR field.)

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Db 187 LVFGLTANSDTHLLQGGSLTLTLESPPGSSPSVQCSPRKNIGGKTLISVSLQELDQSG 246

QY 181 TWICTVLIQNGKVKVEFKIDIV 200

Db 247 TWICTVLIQNGKVKVEFKIDIV 266

## RESULT 89

AAR07640  
ID AAR07640 standard; protein; 2458 AA.

XX AAR07640;

XX 31-OCT-2002 (revised)

DT 20-DEC-1990 (first entry)

XX Deduced protein sequence of p170-2 comprising T4.

DE plasmid p170-2; soluble T4 protein; AIDS; ARC; HIV.

XX Synthetic.

XX Key Location/Qualifiers

FT Protein 400..858

FT /label= T4 surface glycoprotein

FT WO9008198-A.

PN 26-JUL-1990.

PD 18-JAN-1989; 89US-00300096.

XX 18-JAN-1989; 89US-00300096.

XX (HARD ) HARVARD COLLEGE.

XX Letvin NA;

PI WPI; 1990-254040/33.

DR N-PSDB; AAO05607.

XX Treating or preventing AIDS, ARC or HIV infection - by administering an

PT immunologically effective amt. of soluble T4 protein.

XX Disclosure; Fig 1; 121pp; English.

XX Entire sequence from T4-encoding plasmid p170-2. It is almost identical

CC to the sequence published by Maddon et al. (1985) with the exception of

CC three codon changes. At T4 amino acid residue 3, (posn.403 of entire

CC sequence) Lys is encoded in stead of Asn. At posn. 64, (posn.464) Arg

CC replaces Trp and at posn. 231, (posn. 631) Ser replaces Phe. Soluble T4

CC can be produced by truncating the CDS to remove the transmembrane and

CC cytoplasmic domains. The soluble forms may be modified to increase their

CC immunogenicity by addition of an adjuvant such as incomplete Freund's

CC adjuvant. The T4 interferes with HIV/T4 interaction and elicits anti-

CC soluble T4 antibody production. See also AAO05608. (Updated on 31-OCT-

CC 2002 to add missing OS field.)

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QY      121 LVFGLTANSPTLHLGGSLTLTLSPGSSPVQCRSPRGKNIQGGKTLTSSVQLLEIDSG 180
DB      520 LVFGLTANSPTLHLGGSLTLTLSPGSSPVQCRSPRGKNIQGGKTLTSSVQLLEIDSG 579
QY      181 TWCTVLOQNKVKPEFKIDIV 200
DB      580 TWCTVLOQNKVKPEFKIDIV 599

RESULT 90
AAR04031
ID      AAR04031 standard; protein; 2458 AA.
AC      AAR04031;
XX
XX      25-MAR-2003 (revised)
DT      31-OCT-2002 (revised)
DT      29-MAY-1990 (first entry)
XX
XX      Full length T4 encoded by plasmid p170-2.
DE
XX      Soluble T4; p170-2; anti-retroviral agent; AIDS; ARC; HIV; AZT.
KM
XX      Synthetic.
OS
XX      Key Location/Qualifiers
FH      Misc-difference 423
FT      /note= "Trp of Madden et al replaced by Arg"
FT      Misc-difference 425
FT      /note= "Asp of Madden et al replaced by Lys"
FT      Misc-difference 653
FT      /note= "Phe of Madden et al replaced by Ser"
XX
XX      MO8911860-A.
PN
XX      14-DEC-1989.
PD
XX      08-JUN-1989; 89MO-US002453.
PF
XX      10-JUN-1988; 88US-00204645.
PR      20-APR-1989; 89US-00341080.
XX
XX      (BIOU ) BIOGEN NV INC.
PA      (GEHO ) GEN HOSPITAL CORP.
PA      (BIOU ) BIOGEN INC.
PA      (BIOU ) BIOGEN INC.
XX
XX      Fisher RA, Schooley RT, Hirsch MS, Johnson VA, Walker BD;
PI      WPI; 1990-007302/01.
DR      N-PSDB; AAO03005.
XX
XX      Combinations of soluble T4 protein and anti-retroviral agent - having
PT      synergistic activity in treatment and prevention of AIDS, arc and HIV
PT      infection.
XX
XX      Disclosure; Fig 1; 100pp; English.
XX
XX      The sequence differs from that determined by PJ Madden et al., [Cell, 42
CC      PP, 93-104 (1985)] in three places due to three nucleotide substitutions.
CC      The Asp reported at position 3 by Madden et al. was the result of a
CC      sequencing error [DR Litzman et al. Cell, 55, p.541 (1988)]. X = stop
CC      codon. The sequence was deduced from the cDNA insert of p170-2. Soluble
CC      T4 constructs may be produced by truncating this sequence to give
CC      fragments from position 400 to 799, removing the transmembrane and
CC      intracytoplasmic domains whilst retaining the extracellular region
CC      responsible for HIV binding. The sol. T4 is combined with an anti-viral
CC      agent such as AZT. See also AAO03006. (Updated on 31-OCT-2002 to add
CC      missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX      Sequence 2458 AA;
SQ
Query Match      76.6%; Score 1009; DB 2; Length 2458;

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      Best Local Similarity 99.0%; Pred. No. 2,9e-61;
      Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 MKRGVPRHLILVLTALLPATQGNKVYLGKGGPTVELTCASOKKSIOFMKNSNOIK 60
DB      400 MKRGVPRHLILVLTALLPATQGNKVYLGKGGPTVELTCASOKKSIOFMKNSNOIK 459
QY      61 ILNGGSPFLTKGPKSLNBRADSRSLMDQGNPFLIIKNLIKEDSPYICEVEDEKEEYVL 120
DB      460 ILNGGSPFLTKGPKSLNBRADSRSLMDQGNPFLIIKNLIKEDSPYICEVEDEKEEYVL 519
QY      121 LVFGLTANSPTLHLGGSLTLTLSPGSSPVQCRSPRGKNIQGGKTLTSSVQLLEIDSG 180
DB      520 LVFGLTANSPTLHLGGSLTLTLSPGSSPVQCRSPRGKNIQGGKTLTSSVQLLEIDSG 579
QY      181 TWCTVLOQNKVKPEFKIDIV 200
DB      580 TWCTVLOQNKVKPEFKIDIV 599

RESULT 91
AAR04910
ID      AAR04910 standard; protein; 458 AA.
AC      AAR04910;
XX
XX      31-OCT-2002 (revised)
DT      02-OCT-1990 (first entry)
XX
XX      T4 protein as encoded by p170.2.
DE
XX      T4 protein; immunotoxin; Pseudomona endotoxin A; AIDS; HIV; ARC;
KM      angiogenin; fusion protein.
XX
XX      Synthetic.
OS
XX      Key Location/Qualifiers
FH      Peptide 1..26
FT      /label= signal peptide
FT      Protein 27..458
FT      /label= T4 protein
FT      Misc-difference replace(87,N)
FT      /note= "differs from Madden et al"
FT      Misc-difference replace(254,F)
FT      /note= "differs from Madden et al"
XX
XX      MO9004414-A.
PN
XX      03-MAY-1990.
PD
XX      18-OCT-1988; 88US-00259355.
PF
XX      18-OCT-1988; 88US-00259355.
PR      18-OCT-1988; 88US-00259355.
XX
XX      (BIOU ) BIOGEN INC.
PA
XX
XX      Meade HM, Lobb RR, Gates LL, Winkler G;
PI      WPI; 1990-163876/21.
DR      N-PSDB; AAO04555.
XX
XX      New immunotoxin contg. soluble T4 protein components and toxin - esp.
PT      Pseudomonas endotoxin A, for treating or controlling AIDS and related
PT      conditions, and new DNA sequences.
XX
XX      Disclosure; Page 7; -pp; English.
XX
XX      The T4 protein encoded by p170.2 is almost identical to that reported by
CC      P.J. Madden et al [Cell, 42, pp 93-104 (1985)]. The Madden sequence was
CC      revised in 1988 to correct a DNA sequencing error at Aa 3 (corrected from
CC      Asp to Lys; see M12807 in GenBank). The DNA may be truncated (to remove
CC      transmembrane and intracellular regions) and/or modified by SDM, pref. so
CC      the prod. extends from AAs 3-183 of the mature protein. This DNA can then

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CC be ligated to a toxin DNA esp. angiogenin, or a fragment of Pseudomonas  
CC exotoxin A cong. the translocation and ADP-ribosylation domains. The  
CC hybrid DNA can then be inserted into an expression vector and used to  
CC produce recombinant fusion protein which is useful for preventing or  
CC treating AIDS, ARC, and HIV infections. The T4 protein is an HIV receptor  
CC which binds to virus or to infected cells carrying the gp120/160 marker  
CC antigen, so provides v. specific targeting with minimal damage to non-  
CC target cells. (updated on 31-OCT-2002 to add missing OS field.)

XX Sequence 458 AA;

Query Match 76.2%; Score 1004; DB 2; Length 458;

Best Local Similarity 98.5%; Pred. No. 1e-61; Mismatches 0; Gaps 0;

Matches 197; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
    |||||
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEVOL 120
    |||||
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLIQGQSLTTLTSPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180
    |||||
DB 121 LVFGLTANSPTHLIQGQSLTTLTSPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180
QY 181 TWTCVTVLQONQKVEFKIDIV 200
    |||||
DB 181 TWTCVTVLQONQKVEFKIDIV 200
```

#### RESULT 92

AAR11285 AAR11285 standard; protein; 458 AA.

XX AAR11285;

AC 25-MAR-2003 (revised)

DT 09-JAN-2003 (revised)

DT 29-APR-1991 (first entry)

XX DE gp120 binding protein.

XX Human; CD4; AIDS; HIV1; SIV; gp120.

XX Unidentified.

XX Key Location/Qualifiers

FT MISC-difference 59 /label= Thr or Ile

FT MISC-difference 93 /label= Thr or Pro

XX EP414178-A.

XX 27-FEB-1991.

XX 18-AUG-1990; 90EP-00115877.

XX 23-AUG-1989; 89US-00397782.

XX (GEHO ) GEN HOSPITAL CORP.

XX Seed B, Camerini D;

XX WPI; 1991-059419/09.

XX N-PSDB; AAQ10887.

XX New non-human primate and human CD4 or gp120 molecules - used to treat

XX HIV or SIV and immunoglobulin and gp120 binding molecules from new fusion

XX proteins.

PS Claim 17; Page 57; 87pp; English.

XX The fragment from residues 1-134 is also independently claimed. The sub-

CC fragment (and the complete polypeptide) can bind to HIV gp120. See also

CC AAQ10885-6, AAQ10888. (Updated on 09-JAN-2003 to add missing OS field.)

XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 458 AA;

Query Match 76.1%; Score 1002; DB 2; Length 458;

Best Local Similarity 98.0%; Pred. No. 1.4e-61; Mismatches 4; Indels 0; Gaps 0;

Matches 196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
    |||||
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEVOL 120
    |||||
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINKLIKEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLIQGQSLTTLTSPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180
    |||||
DB 121 LVFGLTANSPTHLIQGQSLTTLTSPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180
QY 181 TWTCVTVLQONQKVEFKIDIV 200
    |||||
DB 181 TWTCVTVLQONQKVEFKIDIV 200
```

#### RESULT 93

AAR20151 AAR20151 standard; protein; 399 AA.

XX AAR20151;

AC 25-MAR-2003 (revised)

DT 31-MAR-1992 (first entry)

XX DE Chimpanzee sol. CD4 encoded by pSQ200.

XX Human immunodeficiency virus; HIV; gp 120; AIDS; ARC; glycoprotein;

XX acquired immune deficiency syndrome; AIDS related complex;

XX T helper lymphocytes.

XX Pan troglodytes.

XX Key Location/Qualifiers

FT Peptide 1..25 /label= signal\_sequence

XX WO9118618-A.

XX 12-DEC-1991.

XX 25-MAY-1990; 90US-00529186.

XX 25-MAY-1990; 90US-00529186.

XX (BIOJ ) BIOGEN INC.

XX PI Fisher RA, Hession C, Burkly LC;

XX WPI; 1992-007200/01.

XX N-PSDB; AAQ20326.

XX New immuno-therapeutic human CD4 variants and derivs. - elicit AB

XX production to HIV gp.120, useful in treating, preventing and diagnosing

XX AIDS, ARC and HIV infections.

XX Claim 15; Fig 21; 179pp; English.

XX The sequence was deduced from the DNA sequence of clone pSQ200 which was

CC obcd. by cloning using a reverse transcriptase/PCR amplification  
CC procedure with a non-specific oligo dt to prime first strand synthesis.  
CC The PCR fragments were ligated into sequencing plasmid pNN08 (see  
CC AAQ020326). The DNA sequence can be used to express recombinant soluble CD4  
CC and analogues for use in diagnosis and treatment of diseases caused by  
CC infective agents whose primary targets are T4 lymphocytes. See also  
CC AAR20148-R20155 and AAR21078. (Updated on 25-MAR-2003 to correct PA  
CC field.)  
XX  
XX

SQ Sequence 399 AA;

Query Match 75.9%; Score 999; DB 2; Length 399;  
Best Local Similarity 97.5%; Pred. No. 1,9e-61;

Matches 195; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLQALALPAATQGNKVLGKKGDTVELCTASQKKSIOFHMKNQTK 60  
DB 1 MNRGVPFRHLVLQALALPAATQGNKVLGKKGDTVELCTASQKKSIOFHMKNQTK 60  
QY 61 ILGNQGSFLTQKPSKLNDRADSRSLMDQGNFPLIIKNLIKEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTQKPSKLNDRADSRSLMDQGNFPLIIKNLIKEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSPTHLLOGQSLLTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
DB 121 LVFGLTANSPTHLLOGQSLLTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
QY 181 TWTCTVLQONQKVEFKIDIV 200  
DB 181 TWTCTVLQONQKVEFKIDIV 200

RESULT 94

AAR10988  
ID AAR10988 standard; protein; 458 AA.

XX AC AAR10988;  
XX DT 25-MAR-2003 (revised)  
XX DT 29-APR-1991 (first entry)  
XX DE Chimpanzee CD4 protein.  
XX KM Chimpanzee; CD4; AIDS; HIV1; SIV.  
XX OS Pan troglodytes.  
XX FH Key  
XX FT Protein  
XX FT Location/Qualifiers  
XX FT 26  
XX FT /label= mature CD4  
XX PN EP414178-A.  
XX PD 27-FEB-1991.  
XX PF 18-AUG-1990; 90EP-00115877.  
XX PR 23-AUG-1989; 89US-00397782.  
XX PA (GENO ) GEN HOSPITAL CORP.

XX PI Seed B, Camerini D;  
XX DR WPI; 1991-059419/09.  
XX DR N-PSDB; AAQ10886.

XX PT New non-human primate and human CD4 or gp120 molecules - used to treat  
XX PT HIV or SIV and immunoglobulin and gp120 binding molecules from new fusion  
XX PT proteins.  
XX PS Claim 4; Page 45; 87pp; English.

CC The CD4 protein or HIV gp120-binding fragments of it are used to detect

CC and treat HIV and SIV infection. Animals which can be created include  
CC humans, baboons, orang-utans, chimpanzees, gorillas and rhesus monkeys.  
CC The chimpanzee CD4 is 99 per cent homologous to its human counterpart,  
CC possessing 5 amino acid substitutions in the 433 residue predicted mature  
CC polypeptide. See also AAQ10885, AAQ10887-8. (Updated on 25-MAR-2003 to  
CC correct PA field.)  
XX  
XX

SQ Sequence 458 AA;

Query Match 75.9%; Score 999; DB 2; Length 458;  
Best Local Similarity 97.5%; Pred. No. 2.3e-61;

Matches 195; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLQALALPAATQGNKVLGKKGDTVELCTASQKKSIOFHMKNQTK 60  
DB 1 MNRGVPFRHLVLQALALPAATQGNKVLGKKGDTVELCTASQKKSIOFHMKNQTK 60  
QY 61 ILGNQGSFLTQKPSKLNDRADSRSLMDQGNFPLIIKNLIKEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTQKPSKLNDRADSRSLMDQGNFPLIIKNLIKEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSPTHLLOGQSLLTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
DB 121 LVFGLTANSPTHLLOGQSLLTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
QY 181 TWTCTVLQONQKVEFKIDIV 200  
DB 181 TWTCTVLQONQKVEFKIDIV 200

RESULT 95

AAR20150  
ID AAR20150 standard; protein; 400 AA.

XX AC AAR20150;  
XX DT 25-MAR-2003 (revised)  
XX DT 31-MAR-1992 (first entry)  
XX DE Chimpanzee sol. CD4 sequence from psQ205.  
XX KM Human immunodeficiency virus; HIV; gp 120; AIDS; ARC; glycoprotein;  
XX KM acquired immune deficiency syndrome; AIDS related complex;  
XX OS Pan troglodytes.  
XX FH Key  
XX FT Peptide  
XX FT Location/Qualifiers  
XX FT 1..25  
XX FT /label= signal\_sequence  
XX PN MO9118618-A.  
XX PD 12-DEC-1991.  
XX PF 25-MAY-1990; 90US-00529186.  
XX PR 25-MAY-1990; 90US-00529186.  
XX PA (BIOG ) BIOGEN INC.

XX PI Fisher RA, Hession C, Burkly LC;  
XX DR WPI; 1992-007200/01.  
XX DR N-PSDB; AAQ20325.

XX PT New immuno-therapeutic human CD4 variants and derivs. - elicit AB  
XX PT production to HIV gp.120, useful in treating, preventing and diagnosing  
XX PT AIDS, ARC and HIV infections.  
XX PS Claim 15; Fig 20; 179pp; English.

CC The sequence was deduced from the DNA sequence of clone psQ205 which was

obcd. by cloning using a reverse transcriptase/PCR amplification procedure. The DNA sequence can be used to express recombinant soluble CD4 and analogues for use in diagnosis and treatment of diseases caused by infective agents whose primary targets are T4+ lymphocytes. See also CC AAB20148-R20155 and AAB21078. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 400 AA;

Query Match 75.5%; Score 994; DB 2; Length 400;  
Best Local Similarity 97.0%; Pred. No. 4,36-61;  
Matches 194; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDVVELTCTASOKKSIQFHWKNSNQIK 60  
DB 1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDVVELTCTASOKKSIQFHWKNSNQIK 60  
QY 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSDTHLLOGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSDTHLLOGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCVVLQNKVKVEFKIDIV 200  
DB 181 TWTCVVLQNKVKVEFKIDIV 200

RESULT 96

AAP93010  
ID AAP93010 standard; protein; 399 AA.

XX AAP93010;  
XX 25-MAR-2003 (revised)  
DT 03-AUG-1992 (first entry)  
XX Genetic construct which encodes CD4 linked to human Igm at the Met2 site  
DE upstream of the CH1 region (fusion protein CD4Mmu).  
XX Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;  
KM diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.  
XX Homo sapiens.  
OS  
XX EP325262-A.  
PN  
XX 26-JUL-1989.  
PD  
XX 20-JAN-1989; 89EP-00100913.  
PF  
XX 22-JAN-1988; 88US-00147351.  
PR  
XX (GEHO ) GEN HOSPITAL CORP.  
PA  
XX Seed B;  
PI  
XX WPI; 1989-214472/30.  
DR N-PSDB; AAN90358.  
PT  
XX Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV  
PT infections or detecting HIV or SIV in sample.  
XX  
XX Example; Table 3, Page 34-40; 68pp; English.

The fusion protein genes of the invention pref. comprises cDNA sequences which encode CD4 or a fragment which binds gp120 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene has been deleted (see W087-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The

CC Ig heavy chain is pref. from Igm, IgG1 or IgG3. The following are CC specifically claimed: fusion proteins CD4lambda1, CD4Mmu, CD4Pmu, CC CD4lambda1, and CD4Mmu (No. 67608), PCDA1lambda (No. 67609) and CC PCDA1lambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 399 AA;

Query Match 74.6%; Score 982; DB 1; Length 399;  
Best Local Similarity 97.0%; Pred. No. 2,96-60;  
Matches 194; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDVVELTCTASOKKSIQFHWKNSNQIK 60  
DB 1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDVVELTCTASOKKSIQFHWKNSNQIK 60  
QY 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSDTHLLOGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSDTHLLOGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCVVLQNKVKVEFKIDIV 200  
DB 181 TWTCVVLQNKVKVEFKIDIV 200

RESULT 97

AAB19511  
ID AAB19511 standard; protein; 616 AA.

XX AAB19511;  
XX 09-JAN-2001 (first entry)  
DT  
XX CD4-IgG1 fusion protein CH4Bgammal.  
DE  
XX CD4; IgG1; human; CD4Bgammal; fusion protein; immunoglobulin; HIV; SIV;  
KM gp120; therapy; diagnosis.  
XX Homo sapiens.  
OS  
XX Key  
FT Protein  
FT 1..395 Location/Qualifiers  
FT /note="CD4 extracellular region"  
FT 400..616  
FT /note="IgG1 heavy chain"  
XX  
PN US6117656-A.  
XX  
XX 12-SEP-2000.  
PD  
XX 07-JUN-1995; 95US-00479353.  
PF  
XX 22-JAN-1988; 88US-00147351.  
PR 23-JAN-1989; 89US-00299596.  
PR 09-JUN-1992; 92US-00896781.  
PR 12-APR-1993; 93US-00057952.  
PR 04-FEB-1994; 94US-00191708.  
XX  
XX (GEHO ) GEN HOSPITAL CORP.  
PA  
XX Seed B;  
PI  
XX WPI; 2000-586558/55.  
DR N-PSDB; AAA50664.  
XX  
XX CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV or  
PT SIV.  
XX  
XX Example 1; Col 59-70; 39pp; English.



```
FT /label= fourth Ig-related_domain
FT /note= "extracellular"
FT Disulfide-bond 328..370
FT Domain 396..416
FT /label= hydrophobic/transmembrane_sequence
FT 417..458
FT /label= very_hydrophilic/intracytoplasmic
XX
XX MO9117170-A.
XX
XX 14-NOV-1991.
XX
XX 04-MAY-1990; 90US-00520368.
XX
XX 04-MAY-1990; 90US-00520368.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Peglnsky RB, Rosa MD, Stoesel TP;
XX
XX WPI; 1991-353711/48.
XX N-PSDB; AAQ14931.
XX
XX New multi-meric and hetero-multi-meric geleolin fusion constructs - used
XX to treat and diagnose AIDS, ARC and HIV infection.
XX
XX Disclosure; Fig 3A-3D; 131pp; English.
XX
XX The CD4 polypeptides useful in the constructs include all CD4
XX polypeptides which bind to or otherwise inhibit gp120 and gp160. These
XX include fragments lacking the transmembrane domain. In particular it is
XX CD4 1-111; 1-Cyella; 1-Cyella80; 1-181; 1-183; 1-187; 1-345 or 1-375 (from
XX mature protein). See also AAQ14931-35 and AAR15151. (Updated on 25-MAR-
XX 2003 to correct PA field.)
XX
XX Sequence 458 AA;
SQ
Query March 71.8%; Score 946; DB 2; Length 458;
Best Local Similarity 92.0%; Pred. No. 1,1e-57;
Matches 184; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 MNRGVPRHLLVQLALLPATQGNKVLGKSGDTVELTCTASQKSIQFHMKNQIK 60
DB 1 MNRGVPRHLLVQLALLPATQGNKVLGKSGDTVELTCTASQKSIQFHMKNQIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQL 120
QY 121 LVFGLTANSDPHLLOQGSULTLTSSPSSSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTAKCERDVGERVSLTLERGGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWCTCVLQNKVFEKIDIV 200
DB 181 TWCTCVLQNKVFEKIDIV 200
XX
XX RESULT 100
XX AAP90833
XX ID AAP90833 standard; protein; 384 AA.
XX
XX AAP90833;
XX
XX 25-MAR-2003 (revised)
XX 01-AUG-1990 (first entry)
XX
XX Amino acid sequence of a soluble T4-like (sr4) polypeptide encoded by a
XX portion of clone p199-7 (PL mutet.rst4).
XX HIV; immunotherapeutic; prophylactic; soluble T4-like polypeptide;
XX diagnostic; p199-7 (PL mutet.rst4).
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```
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 10
XX /note= "Initiating Met"
XX
XX MO8901940-A.
XX
XX 09-MAR-1989.
XX
XX 01-SEP-1988; 88WO-US002940.
XX
XX 04-SEP-1987; 87US-00094322.
XX 07-JAN-1988; 88US-00141649.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Fisher RA, Gilbert W, Sato VL, Flavell RA, Maraganore JM;
XX
XX WPI; 1989-085519/11.
XX N-PSDB; AAN90643.
XX
XX DNA sequences coding for soluble T4-like polypeptide(s) - used in
XX immuno:therapeutic and immunosuppressive comps. and for preventing,
XX treating or detecting AIDS.
XX
XX Disclosure; Page 7; 207pp; English.
XX
XX It is the protein sequence encoded by the rst4 sequence. It is claimed in
XX the patent. It is useful in immunotherapeutic, prophylactic and
XX diagnostic comps. It can be used to purify HIV from a sample. (Updated
XX on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 384 AA;
SQ
Query March 69.6%; Score 916; DB 1; Length 384;
Best Local Similarity 100.0%; Pred. No. 1,1e-55;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 QGNKRVVLGKGGDTVELTCTASQKSIQFHMKNQIKILGNQGSFLTKGPKSLNDRADR 83
DB 11 QGNKRVVLGKGGDTVELTCTASQKSIQFHMKNQIKILGNQGSFLTKGPKSLNDRADR 70
QY 84 RSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLVGLTANSDPHLLOQGSULTLT 143
DB 71 RSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLVGLTANSDPHLLOQGSULTLT 130
QY 144 ESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCTVLOQNKVFEKIDIV 200
DB 131 ESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCTVLOQNKVFEKIDIV 187
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Search completed: August 3, 2004, 13:08:20  
Job time : 29.2483 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2004, 13:14:00 ; Search time 21.8374 Seconds

(without alignments)  
3706.029 Million cell updates/sec

Title: SEQ6

Perfect score: 1317

Sequence: 1 MNRGVFRHLLVLQLALLP.....VISFLGLGVACTLARTR 258

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 125 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1038	78.8	310	8	US-08-485-163-7
2	1038	78.8	310	8	US-09-766-995-6
3	1032.5	78.4	432	8	US-08-485-163-3
4	1032.5	78.4	432	8	US-09-766-995-2
5	1030.5	78.2	530	8	US-08-485-163-5
6	1030.5	78.2	530	9	US-09-766-995-4
7	1029	78.1	203	10	US-09-939-537-21
8	1029	78.1	398	10	US-09-939-537-29
9	1029	78.1	402	14	US-10-097-044A-1
10	1029	78.1	457	11	US-09-891-119A-9
11	1029	78.1	462	10	US-09-939-537-5
12	1029	78.1	462	11	US-09-243-008-5
13	1029	78.1	532	10	US-09-939-537-6
14	1029	78.1	532	11	US-09-243-008-6
15	1029	78.1	575	10	US-09-939-537-4

16	1029	78.1	575	11	US-09-243-008-4	Sequence 4, Appli
17	1023	77.7	458	12	US-10-151-274-3	Sequence 3, Appli
18	1023	77.7	458	14	US-10-103-597A-39	Sequence 39, Appli
19	1023	77.7	458	14	US-10-188-444-39	Sequence 39, Appli
20	1021	77.5	458	8	US-10-207-655-170	Sequence 170, App
21	1021	77.5	458	14	US-08-681-219-27	Sequence 27, Appli
22	1021	77.5	458	11	US-09-230-111C-25	Sequence 25, Appli
23	1021	77.5	458	14	US-10-092-138-25	Sequence 25, Appli
24	1012	76.8	397	11	US-09-891-119A-2	Sequence 2, Appli
25	917.5	69.7	448	14	US-10-024-329-32	Sequence 32, Appli
26	916	69.6	434	14	US-10-097-044A-4	Sequence 4, Appli
27	903	68.6	788	14	US-10-073-118-26	Sequence 26, Appli
28	899	68.3	178	9	US-09-934-060A-26	Sequence 26, Appli
29	899	68.3	370	9	US-09-759-841-6	Sequence 6, Appli
30	899	68.3	590	9	US-09-934-060A-13	Sequence 13, Appli
31	899	68.3	720	9	US-09-934-060A-2	Sequence 2, Appli
32	899	68.3	720	9	US-09-934-060A-4	Sequence 4, Appli
33	881	66.9	184	14	US-10-024-329-33	Sequence 33, Appli
34	494	37.5	94	11	US-09-891-119A-10	Sequence 10, Appli
35	486	36.9	93	14	US-10-105-545-26	Sequence 26, Appli
36	475	36.1	612	14	US-10-125-692-10	Sequence 10, Appli
37	337	25.6	84	9	US-09-135-238B-8	Sequence 8, Appli
38	332	25.2	240	9	US-09-997-165-2	Sequence 2, Appli
39	288	21.9	58	10	US-09-939-537-35	Sequence 35, Appli
40	238	18.1	95	14	US-10-105-545-25	Sequence 25, Appli
41	150	11.4	50	14	US-10-076-674-5	Sequence 5, Appli
42	150	11.4	50	14	US-10-355-161A-4	Sequence 4, Appli
43	150	11.4	50	15	US-10-355-161A-5	Sequence 5, Appli
44	150	11.4	50	16	US-10-311-823-13	Sequence 13, Appli
45	139	10.6	570	16	US-10-311-823-13	Sequence 7, Appli
46	139	10.6	535	15	US-10-108-604A-4247	Sequence 4247, Ap
47	133	10.1	1477	14	US-10-274-583-20	Sequence 20, Appli
48	131.5	10.0	1479	12	US-10-231-956A-325	Sequence 35, App
49	131.5	10.0	1496	12	US-10-211-462-87	Sequence 87, Appli
50	131.5	10.0	1496	14	US-10-021-660-125	Sequence 125, App
51	131.5	10.0	1496	15	US-10-331-966A-28	Sequence 28, Appli
52	131.5	10.0	1498	12	US-10-276-177A-1957	Sequence 1957, Ap
53	131.5	10.0	1498	12	US-10-243-552-899	Sequence 899, App
54	131.5	10.0	374	16	US-10-311-823-16	Sequence 16, Appli
55	131	9.9	442	16	US-10-311-823-12	Sequence 12, Appli
56	131	9.9	458	16	US-10-311-823-12	Sequence 4, Appli
57	131	9.9	1260	13	US-10-024-918-27	Sequence 27, Appli
58	131	9.9	1260	16	US-10-650-509-27	Sequence 27, Appli
59	131	9.9	1315	15	US-10-094-886-52	Sequence 52, Appli
60	131	9.9	1386	15	US-10-094-886-38	Sequence 38, Appli
61	131	9.9	338	9	US-09-808-602-69	Sequence 69, Appli
62	129	9.8	338	10	US-09-808-602-69	Sequence 58, Appli
63	129	9.8	338	12	US-10-042-865-92	Sequence 92, Appli
64	129	9.8	338	14	US-10-042-865-92	Sequence 58, Appli
65	129	9.8	338	16	US-10-161-572-58	Sequence 158, App
66	129	9.8	338	9	US-09-808-602-72	Sequence 72, Appli
67	126	9.6	338	10	US-09-800-198-61	Sequence 61, Appli
68	126	9.6	338	12	US-10-042-865-91	Sequence 91, Appli
69	126	9.6	354	12	US-10-042-865-14	Sequence 14, Appli
70	126	9.6	332	9	US-09-989-722-517	Sequence 517, App
71	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
72	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
73	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
74	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
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79	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
80	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
81	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
82	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
83	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
84	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
85	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
86	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
87	125	9.5	332	9	US-09-989-722-517	Sequence 517, App
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Dd		181 TWTCVTLNOKKVERKIDIVLAFTVAAD-----SVFIPEDEQKSGTASY	228
Oy		241 SFL 244	
Dd		229 VCLL 232	
		RESULT 3	
		US-08-485-163-3	
		; Sequence 3, Application US/08485163	
		; Publication No. US20020098191A1	
		GENERAL INFORMATION:	
		APPLICANT: Beauty, Gary A.	
		APPLICANT: Madden, Paul J.	
		TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS	
		NUMBER OF SEQUENCES: 10	
		CORRESPONDENCE ADDRESS:	
		ADDRESSEE: Cooper & Dunham LLP	
		STREET: 1185 Avenue of the Americas	
		CITY: New York	
		STATE: New York	
		COUNTRY: USA	
		ZIP: 10036	
		COMPUTER READABLE FORM:	
		MEDIUM TYPE: Floppy disk	
		COMPUTER: IBM PC compatible	
		OPERATING SYSTEM: PC-DOS/MS-DOS	
		SOFTWARE: Patent In Release #1.24	
		CURRENT APPLICATION DATA:	
		APPLICATION NUMBER: US/08/485,163	
		FILING DATE: 07-JUN-1995	
		CLASSIFICATION: 514	
		ATTORNEY/AGENT INFORMATION:	
		NAME: White, John P.	
		REGISTRATION NUMBER: 28,678	
		REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US	
		TELECOMMUNICATION INFORMATION:	
		TELEPHONE: (212) 278-0400	
		TELEFAX: (212) 391-0525	
		TELEX:	
		INFORMATION FOR SEQ ID NO: 3:	
		SEQUENCE CHARACTERISTICS:	
		LENGTH: 432 amino acids	
		TYPE: amino acid	
		STRANDEDNESS: unknown	
		TOPOLOGY: unknown	
		MOLECULE TYPE: protein	
		ORIGINAL SOURCE:	
		ORGANISM: homo sapien	
		CELL TYPE: lymphocyte	
		US-08-485-163-3	
		Query Match	
		Best Local Similarity 78.4%; Score 1032.5; DB 8; Length 432;	
		Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2	
Oy		1 MRGVDFRHLILVLQALLPAATOGKNVYLKKGDVVELTCTASOKKSIOFHMKNSNQIK	60
Dd		1 MRGVDFRHLILVLQALLPAATOGKVVLLGGKDVELTCTASOKKSIOFHMKNSNQIK	60
Oy		61 ILGNQGSFLTCKPSKLNDRADARRSLMDGNEPLIIKLNKIBDSPIYCEVEEDOKREYOL	120
Dd		61 ILGNQGSFLTCKPSKLNDRADARRSLMDGNEPLIIKLNKIBESDPIYCEVEEQEEYOL	120
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Dd		121 LVFGILTANSDTHTLQGQSILTTLESPPGSSPSVOCSRSPKGNKIQQGKTLSVSQLELDQSG	180
Oy		181 TWTCVTLNOKKVERKIDIV---PRASALPAAPTGSALPDPTASALDDPPAA	230

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DB 181 TWCTCTVLQNGKVEFKIDIVLWAFERKCCVECP-----CPAPVA 221

RESULT 4
US-09-766-995-2
; Sequence 2, Application US/09766995
; Patent No. US20020052481A1
GENERAL INFORMATION:
APPLICANT: Graham P. Allaway et al.
TITLE OF INVENTION: NON-PEPTIDYL NOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJ
FILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 2048/41215-CB/JPM/SHS
CURRENT APPLICATION NUMBER: US/09/766,995
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: homo sapians
US-09-766-995-2

Query Match 78.4%; Score 1032.5; DB 9; Length 432;
Best Local Similarity 88.0%; Pred. No. 5.6e-74;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVPFRHLILVLTQALLPATQGNKRVLGKGDIVELTCTASQKKSIOFHMKNNOIK 60
DB 1 MNRGVPFRHLILVLTQALLPATQGNKRVLGKGDIVELTCTASQKKSIOFHMKNNOIK 60
QY 61 ILGNQGSFLTKGPSKNDRADRSRLWDQNFPLIINLKIETSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPSKNDRADRSRLWDQNFPLIINLKIETSDTYICEVEDQKEEVOL 120
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DB 121 LVFGITANSPTDHLIQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLISVSOLELODSG 180
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RESULT 5
US-08-485-163-5
; Sequence 5, Application US/08485163
; Publication No. US20020098191A1
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,163
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 530 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-485-163-5

Query Match 78.2%; Score 1030.5; DB 8; Length 530;  
Best Local Similarity 84.8%; Pred. No. 1.1e-73;  
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

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DB 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNOIK 60  
QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNLIKIEDSDTYICEVEDQKEEYQL 120  
DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNLIKIEDSDTYICEVEDQKEEYQL 120  
QY 121 LVFGILTANSDTHLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGILTANSDTHLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240  
DB 181 TWTCTVLQNKQKVEFKIDIVLAFASTGK-----SVPLPACNSRSTSTAL 229  
QY 241 SFL 244  
DB 230 GCLV 233

RESULT 6  
US-09-766-995-4  
Sequence 4, Application US/09766995  
Patent No. US20020052481A1  
GENERAL INFORMATION:  
APPLICANT: Graham P. Allaway et al.  
TITLE OF INVENTION: NON-PEPTIDYL MOIEFY-CONJUGATED CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJ  
TITLE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: 2048/41215-CB/JPM/SHS  
CURRENT APPLICATION NUMBER: US/09/766,995  
CURRENT FILING DATE: 2001-01-22  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 530  
TYPE: PRT  
ORGANISM: homo sapians  
US-09-766-995-4

Query Match 78.2%; Score 1030.5; DB 9; Length 530;  
Best Local Similarity 84.8%; Pred. No. 1.1e-73;  
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNOIK 60  
DB 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNOIK 60  
QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNLIKIEDSDTYICEVEDQKEEYQL 120  
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QY 121 LVFGILTANSDTHLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGILTANSDTHLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

DB 121 LVFGILTANSDTHLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
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DB 181 TWTCTVLQNKQKVEFKIDIVLAFASTGK-----SVPLPACNSRSTSTAL 229  
QY 241 SFL 244  
DB 230 GCLV 233

RESULT 7  
US-09-939-537-31  
Sequence 31, Application US/09939537  
Publication No. US20030138410A1  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian  
Banapour, Babak  
Romeo, Charles  
Kolanas, Waldemar  
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED  
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,537  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/284,391  
FILING DATE: 02-AUG-1994  
APPLICATION NUMBER: 08/195,395  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: 07/847,566  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/665,961  
FILING DATE: 07-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Elbing, Karen L.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/247001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 203 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-939-537-31

Query Match 78.1%; Score 1029; DB 10; Length 203;  
Best Local Similarity 100.0%; Pred. No. 4.1e-74;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNOIK 60  
DB 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNOIK 60

QY 61 ILGNQSFLLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120  
DB 61 ILGNQSFLLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120  
QY 121 LVFGLTANSDBTHLLOQOSLTLTLSPSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSDBTHLLOQOSLTLTLSPSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWCTVLOQOKKVEFKIDIV 200  
DB 181 TWCTVLOQOKKVEFKIDIV 200

RESULT 8  
US-09-939-537-29  
Sequence 29, Application US/09939537  
Publication No. US20030138410A1  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian  
Banapour, Babak  
Romeo, Charles  
Kolanus, Waldemar  
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED  
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,537  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/284,391  
FILING DATE: 02-AUG-1994  
APPLICATION NUMBER: 08/195,395  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: 07/847,566  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/665,961  
FILING DATE: 07-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Elbing, Karen L.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/247001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 398 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-939-537-29

Query Match 78.1%; Score 1029; DB 10; Length 398;  
Best Local Similarity 100.0%; Pred. No. 9.7e-74;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMRGVPFHHLLVLTQALLPAATQGNKYVLGKKGDVETLTASQKSIQPFHMKNSNOIK 60  
DB 1 NMRGVPFHHLLVLTQALLPAATQGNKYVLGKKGDVETLTASQKSIQPFHMKNSNOIK 60  
QY 61 ILGNQSFLLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120  
DB 61 ILGNQSFLLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120  
QY 121 LVFGLTANSDBTHLLOQOSLTLTLSPSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSDBTHLLOQOSLTLTLSPSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWCTVLOQOKKVEFKIDIV 200  
DB 181 TWCTVLOQOKKVEFKIDIV 200

RESULT 9  
US-10-097-044A-1  
Sequence 1, Application US/10097044A  
Publication No. US20030143220A1  
GENERAL INFORMATION:  
APPLICANT: Capon, Daniel J.  
Gregory, Timothy J.  
TITLE OF INVENTION: Adhesion Variants  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/097,044A  
FILING DATE: 28-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,918  
FILING DATE: 1-JUN-1995  
APPLICATION NUMBER: 08/236311  
FILING DATE: 02-MAY-1994  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992  
APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubienc, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444P1C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/425-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 402 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-097-044A-1

Query Match 78.1%; Score 1029; DB 14; Length 402;  
Best Local Similarity 100.0%; Pred. No. 9.8e-74;

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MNRGVPFRHLILVQLALIPATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNSQIK 60
    |||
DB 1 MNRGVPFRHLILVQLALIPATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNSQIK 60
    |||
OY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEVOL 120
    |||
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEVOL 120
    |||
OY 121 LVFGLTANSPTHLLOQGSSTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
DB 121 LVFGLTANSPTHLLOQGSSTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
OY 181 TWTCTVLQNOQKVEFKIDIV 200
    |||
DB 181 TWTCTVLQNOQKVEFKIDIV 200
    |||
```

## RESULT 10

US-09-891-119A-9  
Sequence 9, Application US/09891119A  
Publication No. US20040013683A1  
GENERAL INFORMATION:  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4  
FILE REFERENCE: 24577-CY-B  
CURRENT APPLICATION NUMBER: US/09/891,119A  
CURRENT FILING DATE: 2001-06-25  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 457  
TYPE: PRT  
ORGANISM: human  
US-09-891-119A-9

Query Match 78.1%; Score 1029; DB 11; Length 457;  
Best Local Similarity 100.0%; Pred. No. 1,2e-73;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MNRGVPFRHLILVQLALIPATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNSQIK 60
    |||
DB 1 MNRGVPFRHLILVQLALIPATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNSQIK 60
    |||
OY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEVOL 120
    |||
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEVOL 120
    |||
OY 121 LVFGLTANSPTHLLOQGSSTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
DB 121 LVFGLTANSPTHLLOQGSSTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
OY 181 TWTCTVLQNOQKVEFKIDIV 200
    |||
DB 181 TWTCTVLQNOQKVEFKIDIV 200
    |||
```

## RESULT 11

US-09-939-537-5  
Sequence 5, Application US/09939537  
Publication No. US20030138410A1  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian  
Banapour, Babak  
Romeo, Charles  
Kolanus, Waldemar  
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED  
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street

CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/939,537  
FILING DATE: 24-AUG-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284,391  
FILING DATE: 02-AUG-1994  
APPLICATION NUMBER: 08/195,395  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: 07/847,566  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/665,961  
FILING DATE: 07-MAR-1991

## ATTORNEY/AGENT INFORMATION:

NAME: Elbing, Karen L  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/247001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX: <Unknown>

## INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 462 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-939-537-5

Query Match 78.1%; Score 1029; DB 10; Length 462;  
Best Local Similarity 100.0%; Pred. No. 1,2e-73;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MNRGVPFRHLILVQLALIPATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNSQIK 60
    |||
DB 1 MNRGVPFRHLILVQLALIPATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNSQIK 60
    |||
OY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEVOL 120
    |||
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEVOL 120
    |||
OY 121 LVFGLTANSPTHLLOQGSSTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
DB 121 LVFGLTANSPTHLLOQGSSTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
OY 181 TWTCTVLQNOQKVEFKIDIV 200
    |||
DB 181 TWTCTVLQNOQKVEFKIDIV 200
    |||
```

## RESULT 12

US-09-243-008-5  
Sequence 5, Application US/09243008  
Publication No. US20040005334A1  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian et al.  
TITLE OF INVENTION: Redirection of Cellular Immunity by  
Receptor Chimeras  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street

CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: Wordperfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/243,008  
FILING DATE: 02-Feb-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/394,176  
FILING DATE: SEPTEMBER 11, 1995  
APPLICATION NUMBER: 08/203,866  
FILING DATE: February 28, 1994  
APPLICATION NUMBER: 07/847,566  
FILING DATE: March 6, 1992  
APPLICATION NUMBER: 07/665,961  
FILING DATE: March 7, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Karen F. Lech, Ph.D  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/270001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 462 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-243-008-5

Query Match 78.1%; Score 1029; DB 11; Length 462;  
Best Local Similarity 100.0%; Pred. No. 1,2e-73;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMRGVPRHLLVLTQALLPAATQGNKVVLGKKGDVVELTCTASQKSIQPFHMKNSNQIK 60  
DB 1 NMRGVPRHLLVLTQALLPAATQGNKVVLGKKGDVVELTCTASQKSIQPFHMKNSNQIK 60  
QY 61 ILGNQSPFLTKGSPKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEYQL 120  
DB 61 ILGNQSPFLTKGSPKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEYQL 120  
QY 121 LVFGLTANSDDTHLLQGQSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSDDTHLLQGQSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCTVLONQKKVEFKIDIV 200  
DB 181 TWTCTVLONQKKVEFKIDIV 200

RESULT 13  
US-09-939-537-6  
Sequence 6, Application US/09939537  
Publication No. US20030138410A1  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian  
Banapour, Babak  
Kojanus, Charles  
Romeo, Waldemar  
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED  
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP

STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,537  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/284,391  
FILING DATE: 02-AUG-1994  
APPLICATION NUMBER: 08/195,395  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: 07/847,566  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/665,961  
FILING DATE: 07-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Elbing, Karen L  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/247001  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-939-537-6

Query Match 78.1%; Score 1029; DB 10; Length 532;  
Best Local Similarity 100.0%; Pred. No. 1,4e-73;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMRGVPRHLLVLTQALLPAATQGNKVVLGKKGDVVELTCTASQKSIQPFHMKNSNQIK 60  
DB 1 NMRGVPRHLLVLTQALLPAATQGNKVVLGKKGDVVELTCTASQKSIQPFHMKNSNQIK 60  
QY 61 ILGNQSPFLTKGSPKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEYQL 120  
DB 61 ILGNQSPFLTKGSPKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEYQL 120  
QY 121 LVFGLTANSDDTHLLQGQSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSDDTHLLQGQSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCTVLONQKKVEFKIDIV 200  
DB 181 TWTCTVLONQKKVEFKIDIV 200

RESULT 14  
US-09-243-008-6  
Sequence 6, Application US/09243008  
Publication No. US20040005334A1  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian et al.  
Receptor Chimeras  
TITLE OF INVENTION: Redirection of Cellular Immunity by  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: Wordperfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/243,008  
FILING DATE: 02-Feb-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/394,176  
FILING DATE: SEPTEMBER 11, 1995  
APPLICATION NUMBER: 08/203,866  
FILING DATE: February 28, 1994  
APPLICATION NUMBER: 07/847,566  
FILING DATE: March 6, 1992  
APPLICATION NUMBER: 07/665,961  
FILING DATE: March 7, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Karen F. Lech, Ph.D  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/270001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 532 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-243-008-6  
Query Match 78.1%; Score 1029; DB 11; Length 532;  
Best Local Similarity 100.0%; Pred. No. 1.4e-73;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNRGVPFRHLILVQLALPAPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNOIK 60  
DB 1 MNRGVPFRHLILVQLALPAPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNOIK 60  
QY 61 ILNGGSEFLTKGPKSLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVQL 120  
DB 61 ILNGGSEFLTKGPKSLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVQL 120  
QY 121 LVFGILTANSDTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGILTANSDTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCTVLOQKQKVEFKIDIV 200  
DB 181 TWTCTVLOQKQKVEFKIDIV 200  
RESULT 15  
US-09-939-537-4  
Sequence 4, Application US/09939537  
Publication No. US20030138410A1  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian  
Banapour, Babak  
Romeo, Charles  
Kolanus, Waldemar  
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED  
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,537  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/284,391  
FILING DATE: 02-AUG-1994  
APPLICATION NUMBER: 08/195,395  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: 07/847,566  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/665,961  
FILING DATE: 07-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Elbing, Karen L  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/247001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 575 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-939-537-4  
Query Match 78.1%; Score 1029; DB 10; Length 575;  
Best Local Similarity 100.0%; Pred. No. 1.5e-73;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNRGVPFRHLILVQLALPAPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNOIK 60  
DB 1 MNRGVPFRHLILVQLALPAPATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNSNOIK 60  
QY 61 ILNGGSEFLTKGPKSLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVQL 120  
DB 61 ILNGGSEFLTKGPKSLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVQL 120  
QY 121 LVFGILTANSDTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGILTANSDTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCTVLOQKQKVEFKIDIV 200  
DB 181 TWTCTVLOQKQKVEFKIDIV 200  
RESULT 16  
US-09-243-008-4  
Sequence 4, Application US/09243008  
Publication No. US20040005334A1  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian et al.  
TITLE OF INVENTION: Redirection of Cellular Immunity by  
Receptor Chimeras  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESSES:

```
/ ADDRESS: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ OPERATING SYSTEM: IBM PC/2 Model 502 or 55SX
/ SOFTWARE: Wordperfect (Version 5.0)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/243,008
/ FILING DATE: 02-Feb-1999
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US/08/394,176
/ FILING DATE: SEPTEMBER 11,1995
/ APPLICATION NUMBER: 08/203,866
/ FILING DATE: February 28, 1994
/ APPLICATION NUMBER: 07/847,566
/ FILING DATE: March 6, 1992
/ APPLICATION NUMBER: 07/665,961
/ FILING DATE: March 7, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Karen F. Lech, Ph.D
/ REGISTRATION NUMBER: 35,238
/ REFERENCE/DOCKET NUMBER: 00786/270001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 575 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-243-008-4

Query Match
Best Local Similarity 78.1%; Score 1029; DB 11; Length 575;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALPPATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNSQIK 60
DB 1 MNRGVPRHLLVQLALPPATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNSQIK 60
QY 61 ILGNQGSFLTKGPSKLNDRADRSRLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQGSFLTKGPSKLNDRADRSRLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
QY 121 LVFGILTANSDTHLLOQGSILTLTLESPGSSPSVOCRSBRGNIOGKTLVSQLELDQSG 180
DB 121 LVFGILTANSDTHLLOQGSILTLTLESPGSSPSVOCRSBRGNIOGKTLVSQLELDQSG 180
QY 181 TWTCTVLONQKKVEFKIDIV 200
DB 181 TWTCTVLONQKKVEFKIDIV 200

RESULT 17
US-10-151-274-3
/ Sequence 3, Application US/10151274
/ Publication No. US20030064071A1
/ GENERAL INFORMATION:
/ APPLICANT: Liltman, Dan R.
/ APPLICANT: Kwon, Douglas S.
/ APPLICANT: van Kooyk, Yvette
/ APPLICANT: Geilendeck, Theo
/ TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
/ TITLE OF INVENTION: INTO
/ TITLE OF INVENTION: CELLS
```

```
/ FILE REFERENCE: 1049-1-017
/ CURRENT APPLICATION NUMBER: US/10/151,274
/ CURRENT FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: US/09/517,605
/ PRIOR FILING DATE: 2000-03-02
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 3
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-151-274-3

Query Match
Best Local Similarity 77.7%; Score 1023; DB 12; Length 458;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALPPATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNSQIK 60
DB 1 MNRGVPRHLLVQLALPPATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNSQIK 60
QY 61 ILGNQGSFLTKGPSKLNDRADRSRLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQGSFLTKGPSKLNDRADRSRLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
QY 121 LVFGILTANSDTHLLOQGSILTLTLESPGSSPSVOCRSBRGNIOGKTLVSQLELDQSG 180
DB 121 LVFGILTANSDTHLLOQGSILTLTLESPGSSPSVOCRSBRGNIOGKTLVSQLELDQSG 180
QY 181 TWTCTVLONQKKVEFKIDIV 200
DB 181 TWTCTVLONQKKVEFKIDIV 200
```

```
RESULT 18
US-10-103-597A-39
/ Sequence 39, Application US/10103597A
/ Publication No. US20030096432A1
/ GENERAL INFORMATION:
/ APPLICANT: Jakobsen, Bent Karsten
/ TITLE OF INVENTION: Screening Methods
/ FILE REFERENCE: 102286.142
/ CURRENT APPLICATION NUMBER: US/10/103,597A
/ CURRENT FILING DATE: 2002-10-17
/ PRIOR APPLICATION NUMBER: PCT/GB00/03579
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: GB 9922352.1
/ PRIOR FILING DATE: 1999-09-21
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 39
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-103-597A-39

Query Match
Best Local Similarity 77.7%; Score 1023; DB 14; Length 458;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALPPATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNSQIK 60
DB 1 MNRGVPRHLLVQLALPPATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNSQIK 60
QY 61 ILGNQGSFLTKGPSKLNDRADRSRLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQGSFLTKGPSKLNDRADRSRLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
QY 121 LVFGILTANSDTHLLOQGSILTLTLESPGSSPSVOCRSBRGNIOGKTLVSQLELDQSG 180
DB 121 LVFGILTANSDTHLLOQGSILTLTLESPGSSPSVOCRSBRGNIOGKTLVSQLELDQSG 180
QY 181 TWTCTVLONQKKVEFKIDIV 200
```

```
Db 181 TWCTVVLQNKVKVEFKIDIV 200
|||||
RESULT 19
US-10-188-444-39
; Sequence 39, Application US/10188444
; Publication No. US20030104635A1
; GENERAL INFORMATION:
; APPLICANT: Jakobson, Bent Karsten
; TITLE OF INVENTION: Screening Methods
; FILE REFERENCE: 102286.142 (CIP)
; CURRENT APPLICATION NUMBER: US/10/188,444
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: PCT/GB00/03579
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 9922352.1
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-444-39

Query Match 77.7%; Score 1023; DB 14; Length 458;
Best Local Similarity 99.5%; Pred. No. 3.5e-73;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALLPATQGNKVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
Db 1 MNRGVPFRHLILVQLALLPATQGNKVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
QY 61 ILGNQGSFLTIGKPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120
|||||
Db 61 ILGNQGSFLTIGKPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120
|||||
QY 121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
|||||
Db 121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
|||||
QY 181 TWCTVVLQNKVKVEFKIDIV 200
|||||
Db 181 TWCTVVLQNKVKVEFKIDIV 200
|||||

RESULT 20
US-10-207-655-170
; Sequence 170, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 170
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-170

Query Match 77.7%; Score 1023; DB 14; Length 458;
Best Local Similarity 99.5%; Pred. No. 3.5e-73;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALLPATQGNKVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
Db 1 MNRGVPFRHLILVQLALLPATQGNKVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
```

```
QY 61 ILGNQGSFLTIGKPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120
|||||
Db 61 ILGNQGSFLTIGKPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120
|||||
QY 121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
|||||
Db 121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
|||||
QY 181 TWCTVVLQNKVKVEFKIDIV 200
|||||
Db 181 TWCTVVLQNKVKVEFKIDIV 200
|||||

RESULT 21
US-08-681-219-27
; Sequence 27, Application US/08681219
; Publication No. US20020058607A1
; GENERAL INFORMATION:
; APPLICANT: Takaaki Sato and Junn Yanagisawa
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
; TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
; TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/48962/JPW/JKM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-681-219-27

Query Match 77.5%; Score 1021; DB 8; Length 458;
Best Local Similarity 99.0%; Pred. No. 5e-73;
Matches 198; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALLPATQGNKVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
Db 1 MNRGVPFRHLILVQLALLPATQGNKVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
QY 61 ILGNQGSFLTIGKPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120
|||||
Db 61 ILGNQGSFLTIGKPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120
|||||
QY 121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
|||||
Db 121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
|||||
QY 181 TWCTVVLQNKVKVEFKIDIV 200
|||||
```



Db 181 TWCTVLOKQKVEFKIDIV 200

## RESULT 22

US-09-230-111C-25  
; Sequence 25, Application US/09230111C  
; Publication No. US20030203414A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Taka-Aki  
; APPLICANT: Yanoigisawa, Junn  
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN  
; SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)  
; TITLE OF INVENTION: DOMAIN AND USES THEREOF  
; FILE REFERENCE: 48962-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/230,111C  
; CURRENT FILING DATE: 1999-05-17  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: human  
US-09-230-111C-25

Query Match 77.5%; Score 1021; DB 11; Length 458;

Best Local Similarity 99.0%; Pred. No. 5e-73;

Matches 198; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNRGVPFRHLILVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Db 1 MNRGVPFRHLILVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Qy 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMKIEDSDTYICEVEDQKEEVQL 120

Db 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMKIEDSDTYICEVEDQKEEVQL 120

Qy 121 LVFGLTANSDFHLLQGGSLTTLTSSPPSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Db 121 LVFGLTANSDFHLLQGGSLTTLTSSPPSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Qy 181 TWCTVLOKQKVEFKIDIV 200

Db 181 TWCTVLOKQKVEFKIDIV 200

RESULT 23

US-10-092-138-25  
; Sequence 25, Application US/10092138  
; Publication No. US20030170723A1

; GENERAL INFORMATION:  
; APPLICANT: Sato, Taka-Aki

; TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON

; FILE REFERENCE: 65823/JPW/PT

; CURRENT APPLICATION NUMBER: US/10/092,138

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 458

; TYPE: PRT

; ORGANISM: human

US-10-092-138-25

Query Match 77.5%; Score 1021; DB 14; Length 458;

Best Local Similarity 99.0%; Pred. No. 5e-73;

Matches 198; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNRGVPFRHLILVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Db 1 MNRGVPFRHLILVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Qy 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMKIEDSDTYICEVEDQKEEVQL 120

Db 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMKIEDSDTYICEVEDQKEEVQL 120

Qy 121 LVFGLTANSDFHLLQGGSLTTLTSSPPSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Db 121 LVFGLTANSDFHLLQGGSLTTLTSSPPSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Qy 181 TWCTVLOKQKVEFKIDIV 200

Db 181 TWCTVLOKQKVEFKIDIV 200

RESULT 24

US-09-891-119A-2  
; Sequence 2, Application US/09891119A  
; Publication No. US20040013683A1

; GENERAL INFORMATION:  
; APPLICANT: Maddon, Paul J.

; TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4

; FILE REFERENCE: 24577-CY-B

; CURRENT APPLICATION NUMBER: US/09/891,119A

; CURRENT FILING DATE: 2001-06-25

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 397

; TYPE: PRT

; ORGANISM: Human

US-09-891-119A-2

Query Match 76.8%; Score 1012; DB 11; Length 397;

Best Local Similarity 98.5%; Pred. No. 2.2e-72;

Matches 197; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNRGVPFRHLILVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Db 1 MNRGVPFRHLILVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Qy 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMKIEDSDTYICEVEDQKEEVQL 120

Db 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMKIEDSDTYICEVEDQKEEVQL 120

Qy 121 LVFGLTANSDFHLLQGGSLTTLTSSPPSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Db 121 LVFGLTANSDFHLLQGGSLTTLTSSPPSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Qy 181 TWCTVLOKQKVEFKIDIV 200

Db 181 TWCTVLOKQKVEFKIDIV 200

RESULT 25

US-10-024-329-32  
; Sequence 32, Application US/10024329  
; Publication No. US20030157063A1

; GENERAL INFORMATION:  
; APPLICANT: SANHADJI, Kamel

; APPLICANT: TOURAINE, Jean-Louis

; APPLICANT: LEROY, Pierre

; APPLICANT: MEHRALI, Majid

; TITLE OF INVENTION: Gene therapy using anti-gp41 antibody and cd4 immunoadhesin

; FILE REFERENCE: 109993

; CURRENT APPLICATION NUMBER: US/10/024,329

; CURRENT FILING DATE: 2001-12-21

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 32

; LENGTH: 448

; TYPE: PRT

; ORGANISM: human scd4

US-10-024-329-32

Query Match 69.7%; Score 917.5; DB 14; Length 448;  
Best Local Similarity 95.5%; Pred. No. 8.7e-65;  
Matches 191; Conservative 0; Mismatches 2; Indels 7; Gaps 6;

QY 1 MNRGVPFRLHLVLTALIPATQGNKYLGGKGTVELTCTASQKSIQFHMKNNOIK 60  
DB 1 MNRGVPF-HLLVLTALIPATQGNKYLGGKGTVELTCTASQKSIQFHMKNNOIK 59  
QY 61 ILGNQGSFLTGPSTKLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVQL 120  
DB 60 ILGNQGSFLTGPSTKLNDRADSRSLMDQGNFPLIINKLIEDSDTYIC--VDQKEEVQL 117  
QY 121 LVFGLTANSDBTHLQGSGLTTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 118 LVFGLTANSDBTHLQGSGLTTLTLESPPGSSPVQCRSPR-KNI-QGKTLVS-LQLDQSG 174  
QY 181 TWTCTVLONQKVEFKIDIV 200  
DB 175 TWTCTVLON-KKVEFKIDIV 193

RESULT 26  
US-10-097-044A-4  
; Sequence 4, Application US/10097044A  
; Publication No. US20030143220A1  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; Gregory, Timothy J.  
; TITLE OF INVENTION: Adhesion Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/097,044A  
; FILING DATE: 28-May-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/457,918  
; FILING DATE: 1-JUN-1995  
; APPLICATION NUMBER: 08/236311  
; FILING DATE: 02-MAY-1994  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.  
; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P0444P1C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-8228  
; TELEFAX: 415/952-9681  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 434 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-097-044A-4  
Query Match 69.6%; Score 916; DB 14; Length 434;  
Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 QGNRYVLGGKGDVLTCTASQKSIQFHMKNNOIKILGNQGSFLTGPSTKLNDRADSR 83  
DB 56 QGNRYVLGGKGDVLTCTASQKSIQFHMKNNOIKILGNQGSFLTGPSTKLNDRADSR 115  
QY 84 RSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVQLVGLTANSDBTHLQGSGLTTL 143  
DB 116 RSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVQLVGLTANSDBTHLQGSGLTTL 175  
QY 144 ESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLONQKVEFKIDIV 200  
DB 176 ESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLONQKVEFKIDIV 232

RESULT 27  
US-10-073-118-26  
; Sequence 26, Application US/10073118  
; Publication No. US2003005454A1  
; GENERAL INFORMATION:  
; APPLICANT: BECOUART, JEROME  
; TITLE OF INVENTION: ALBUMIN DERIVATIVES WITH THERAPEUTIC FUNCTIONS  
; FILE REFERENCE: 06832.1429-03  
; CURRENT APPLICATION NUMBER: US/10/073,118  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 09/551,635  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 09/004,319  
; PRIOR FILING DATE: 1998-01-08  
; PRIOR APPLICATION NUMBER: 08/479,146  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/295,078  
; PRIOR FILING DATE: 1994-08-26  
; PRIOR APPLICATION NUMBER: 08/121,236  
; PRIOR FILING DATE: 1993-09-13  
; PRIOR APPLICATION NUMBER: 07/955,243  
; PRIOR FILING DATE: 1992-10-01  
; PRIOR APPLICATION NUMBER: 07/561,879  
; PRIOR FILING DATE: 1990-08-02  
; PRIOR APPLICATION NUMBER: FR 89 10480  
; PRIOR FILING DATE: 1989-08-03  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 788  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Protein fusion  
; OTHER INFORMATION: Prepro-HSA-V1V2  
US-10-073-118-26  
Query Match 68.6%; Score 903; DB 14; Length 788;  
Best Local Similarity 95.7%; Pred. No. 2.6e-63;  
Matches 178; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 19 LPAATGQ---NKVVLGGKGDVLTCTASQKSIQFHMKNNOIKILGNQGSFLTGPSTK 74  
DB 599 LVAASQALGLKTVLGGKGDVLTCTASQKSIQFHMKNNOIKILGNQGSFLTGPSTK 658  
QY 75 KLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVQLVGLTANSDBTHL 134  
DB 659 KLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVQLVGLTANSDBTHL 718  
QY 135 QGGSGLTTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLONQKVE 194  
DB 719 QGGSGLTTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLONQKVE 778  
QY 195 FKIDIV 200

Db 779 FKIDIV 784

## RESULT 28

US-09-934-060A-26  
Sequence 26, Application US/09934060A  
Patent No. US20020155121A1  
GENERAL INFORMATION:  
APPLICANT: Devico, Anthony L.  
APPLICANT: Fouts, Timothy R.  
APPLICANT: Tuskan, Robert G.  
TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE  
FILE REFERENCE: 4115-144 CIP  
CURRENT APPLICATION NUMBER: US/09/934,060A  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: US 09/684,026  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 60/158,321  
PRIOR FILING DATE: 1999-10-08  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 26  
LENGTH: 178  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized construct  
US-09-934-060A-26

Query Match 68.3%; Score 899; DB 9; Length 178;  
Best Local Similarity 100.0%; Pred. No. 8,1e-64;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KVLGKGGDTVELTCTASOKKSIOFHMKNSNOIKILNGSFLTKGPKSLNDRADSRSL 86  
DB 2 KVLGKGGDTVELTCTASOKKSIOFHMKNSNOIKILNGSFLTKGPKSLNDRADSRSL 61  
QY 87 WDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQVLVFGLTANSPTHLLQGOSLTTLTLESP 146  
DB 62 WDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQVLVFGLTANSPTHLLQGOSLTTLTLESP 121  
QY 147 PSSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCTVLOKQKVEFKIDIV 200  
DB 122 PSSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCTVLOKQKVEFKIDIV 175

## RESULT 29

US-09-759-841-6  
Sequence 6, Application US/09759841  
Patent No. US20010039026A1  
GENERAL INFORMATION:  
APPLICANT: Rickett, Graham A  
APPLICANT: Dobbs, Susan  
APPLICANT: Perros, Manousos  
TITLE OF INVENTION: Aasey Method  
FILE REFERENCE: PC103484PME  
CURRENT APPLICATION NUMBER: US/09/759,841  
CURRENT FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: GB 0000664.9  
PRIOR FILING DATE: 2000-01-12  
PRIOR APPLICATION NUMBER: GB 0000663.5  
PRIOR FILING DATE: 2000-01-12  
PRIOR APPLICATION NUMBER: GB 0000659.3  
PRIOR FILING DATE: 2000-01-12  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 370  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-759-841-6

Query Match 68.3%; Score 899; DB 9; Length 370;  
Best Local Similarity 100.0%; Pred. No. 2e-63;  
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KVLGKGGDTVELTCTASOKKSIOFHMKNSNOIKILNGSFLTKGPKSLNDRADSRSL 86  
DB 2 KVLGKGGDTVELTCTASOKKSIOFHMKNSNOIKILNGSFLTKGPKSLNDRADSRSL 61  
QY 87 WDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQVLVFGLTANSPTHLLQGOSLTTLTLESP 146  
DB 62 WDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQVLVFGLTANSPTHLLQGOSLTTLTLESP 121  
QY 147 PSSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCTVLOKQKVEFKIDIV 200  
DB 122 PSSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCTVLOKQKVEFKIDIV 175

## RESULT 30

US-09-934-060A-13  
Sequence 13, Application US/09934060A  
Patent No. US20020155121A1  
GENERAL INFORMATION:  
APPLICANT: Devico, Anthony L.  
APPLICANT: Fouts, Timothy R.  
APPLICANT: Tuskan, Robert G.  
TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE  
FILE REFERENCE: 4115-144 CIP  
CURRENT APPLICATION NUMBER: US/09/934,060A  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: US 09/684,026  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 60/158,321  
PRIOR FILING DATE: 1999-10-08  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 13  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthesized construct  
NAME/KEY: MISC FEATURE  
LOCATION: (586), (586)  
OTHER INFORMATION: Xaa can be any amino acid  
NAME/KEY: MISC FEATURE  
LOCATION: (589), (589)  
OTHER INFORMATION: Xaa can be any amino acid  
US-09-934-060A-13

Query Match 68.3%; Score 899; DB 9; Length 590;  
Best Local Similarity 100.0%; Pred. No. 3.7e-63;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KVLGKGGDTVELTCTASOKKSIOFHMKNSNOIKILNGSFLTKGPKSLNDRADSRSL 86  
DB 399 KVLGKGGDTVELTCTASOKKSIOFHMKNSNOIKILNGSFLTKGPKSLNDRADSRSL 458  
QY 87 WDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQVLVFGLTANSPTHLLQGOSLTTLTLESP 146  
DB 459 WDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQVLVFGLTANSPTHLLQGOSLTTLTLESP 518  
QY 147 PSSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCTVLOKQKVEFKIDIV 200  
DB 519 PSSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCTVLOKQKVEFKIDIV 572

## RESULT 31

US-09-934-060A-2  
Sequence 2, Application US/09934060A  
Patent No. US20020155121A1  
GENERAL INFORMATION:  
APPLICANT: Devico, Anthony L.  
APPLICANT: Fouts, Timothy R.

```

; APPLICANT: Tuskan, Robert G.
; TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE
; FILE REFERENCE: 4115-144 CIP
; CURRENT APPLICATION NUMBER: US/09/934,060A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/684,026
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/158,321
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized construct
; NAME/KEY: MISC_FEATURE
; LOCATION: (716)..(716)
; OTHER INFORMATION: Xaa can be any amino acid
; NAME/KEY: MISC_FEATURE
; LOCATION: (719)..(719)
; OTHER INFORMATION: Xaa can be any amino acid
; US-09-934-060A-2

```

```

Query Match          68.3%; Score 899; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 4,8e-63;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 27 KVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNQGSFLTKGPSKLNDRADSRSL 86
    |||||||
DB 529 KVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNQGSFLTKGPSKLNDRADSRSL 588
    |||||||
QY 87 WDGNFPLIKNLKIEDSDTYICEVEDQKEVQLLVFGLTANSDPHLLQGOSLTLTLESP 146
    |||||||
DB 589 WDGNFPLIKNLKIEDSDTYICEVEDQKEVQLLVFGLTANSDPHLLQGOSLTLTLESP 648
    |||||||
QY 147 PGSSPSVQCRSPRGKNIQGGKTLVSQLELDSDGTWCTVLOKQKVEFKIDIV 200
    |||||||
DB 649 PGSSPSVQCRSPRGKNIQGGKTLVSQLELDSDGTWCTVLOKQKVEFKIDIV 702
    |||||||

```

```

RESULT 32
US-09-934-060A-4
; Sequence 4, Application US/09934060A
; Patent No. US20020155121A1
; GENERAL INFORMATION:
; APPLICANT: Devico, Anthony L.
; APPLICANT: Fouts, Timothy R.
; APPLICANT: Tuskan, Robert G.
; TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE
; FILE REFERENCE: 4115-144 CIP
; CURRENT APPLICATION NUMBER: US/09/934,060A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/684,026
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/158,321
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized construct
; NAME/KEY: MISC_FEATURE
; LOCATION: (716)..(716)
; OTHER INFORMATION: Xaa can be any amino acid
; NAME/KEY: MISC_FEATURE
; LOCATION: (719)..(719)
; OTHER INFORMATION: Xaa can be any amino acid
; US-09-934-060A-4

```

```

Query Match          68.3%; Score 899; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 4,8e-63;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 27 KVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNQGSFLTKGPSKLNDRADSRSL 86
    |||||||
DB 529 KVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNQGSFLTKGPSKLNDRADSRSL 588
    |||||||
QY 87 WDGNFPLIKNLKIEDSDTYICEVEDQKEVQLLVFGLTANSDPHLLQGOSLTLTLESP 146
    |||||||
DB 589 WDGNFPLIKNLKIEDSDTYICEVEDQKEVQLLVFGLTANSDPHLLQGOSLTLTLESP 648
    |||||||
QY 147 PGSSPSVQCRSPRGKNIQGGKTLVSQLELDSDGTWCTVLOKQKVEFKIDIV 200
    |||||||
DB 649 PGSSPSVQCRSPRGKNIQGGKTLVSQLELDSDGTWCTVLOKQKVEFKIDIV 702
    |||||||

```

```

RESULT 33
US-10-024-329-33
; Sequence 33, Application US/10024329
; Publication No. US20030157063A1
; GENERAL INFORMATION:
; APPLICANT: SANHADJI, Kamel
; APPLICANT: TOURAINE, Jean-Louis
; APPLICANT: LEROY, Pierre
; APPLICANT: MEHTALI, Majid
; TITLE OF INVENTION: Gene therapy using anti-gp11 antibody and cd4 immunoadhesin
; FILE REFERENCE: 109993
; CURRENT APPLICATION NUMBER: US/10/024,329
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 184
; TYPE: PRT
; ORGANISM: L, D1, J1, D2 domains of human bCD4
; US-10-024-329-33

```

```

Query Match          66.9%; Score 881; DB 14; Length 184;
Best Local Similarity 95.3%; Pred. No. 2,3e-62;
Matches 181; Conservative 1; Mismatches 2; Indels 6; Gaps 5;

```

```

QY 1 MNRGVPFRHLIVQLLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHWNKSNQIK 60
    |||||||
DB 1 MNRGVPFRHLIVQLLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHWNKSNQIK 59
    |||||||
QY 61 ILNQGSFLTKGPSKLNDRADSRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEVQL 120
    |||||||
DB 60 ILNQGSFLTKGPSKLNDRADSRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEVQL 117
    |||||||
QY 121 LVFGLTANSDPHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDSDG 180
    |||||||
DB 118 LVFGLTANSDPHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDSDG 174
    |||||||
QY 181 TWCTVLOKQ 190
    |||||||
DB 175 TWCTVLOKQ 184
    |||||||

```

```

RESULT 34
US-09-891-119A-10
; Sequence 10, Application US/09891119A
; Publication No. US20040013683A1
; GENERAL INFORMATION:
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
; FILE REFERENCE: 24577-CY-B
; CURRENT APPLICATION NUMBER: US/09/891,119A
; CURRENT FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10

```

LENGTH: 94  
TYPE: PRT  
ORGANISM: human  
US-09-891-119A-10

Query Match 37.5%; Score 494; DB 11; Length 94;  
Best Local Similarity 100.0%; Pred. No. 7e-32;

Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 QGNKVLGKGGDTVELTCTASQKSIQFHWKNSNOIKILGSGFLTKGPSKLANDRADR 83  
DB 1 QGNKVLGKGGDTVELTCTASQKSIQFHWKNSNOIKILGSGFLTKGPSKLANDRADR 60  
QY 84 RSLMDGNFPLIIKNLKIEDSDTYICEVEDOKEE 117  
DB 61 RSLMDGNFPLIIKNLKIEDSDTYICEVEDOKEE 94

RESULT 35  
US-10-105-545-26

Sequence 26, Application US/10105545  
Publication No. US20030144479A1

GENERAL INFORMATION:

APPLICANT: Mark, Greene I.

APPLICANT: William, William V.

APPLICANT: Weiner, David B.

APPLICANT: Cohen, Jeffrey A.

APPLICANT: Kieber-Bemmons, Thomas

APPLICANT: Williams, Robert M.

APPLICANT: Williams, Robert M.

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APPLICANT: Williams, Robert M.

APPLICANT: Williams, Robert M.

QY 77 NDRADRSRLMDGNFPLIIKNLKIEDSDTYIC 109  
DB 61 NDRADRSRLMDGNFPLIIKNLKIEDSDTYIC 93

RESULT 36  
US-10-125-692-10

Sequence 10, Application US/10125692  
Publication No. US20030044429A1

GENERAL INFORMATION:

APPLICANT: Ademem, Alan

APPLICANT: Hayashi, Fumitaka

APPLICANT: Smith, Kelly D.

APPLICANT: Underhill, David M.

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

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APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

US-10-125-692-10

Query Match 36.1%; Score 475; DB 14; Length 612;  
Best Local Similarity 52.8%; Pred. No. 2.5e-29;

Matches 104; Conservative 32; Mismatches 55; Indels 6; Gaps 5;

QY 1 MNRGVPFRH-LLVLQALLPAPATQGNKVLGKGGDTVELTCTASQKSIQFHWKNSNOI 59  
DB 1 MCRATSRRLRLLLQLQSLAVTQKTLVKGESALPCESSQKKTIVFTWFSQDR 60  
QY 60 KILGNG-SFLTGG-PPKLANDRADSRLMDGNFPLIIKNLKIEDSDTYICEVEDOKE 116  
DB 61 KILGNGHGVLRGSPSQF-DREDSKGAWEKGFPLIKNLKIEDSDTYICELENRKE 119  
QY 117 EVOLVFLTANSDPHLQGSLLTLES-PPGSSPSVQCSPPCKNIQGGKTLSSVSOLE 175  
DB 120 EVELWVFVTFSPGSLQGSLLTLDNSKNSNPLTECHGKGVSSKVLMSNLR 179  
QY 176 LODSGTWTCTVLQNGK 192  
DB 180 VQSDSFNCTVTLQDK 196

RESULT 37  
US-09-135-238B-8

Sequence 8, Application US/09135238B  
Patent No. US2002017565A1

GENERAL INFORMATION:

APPLICANT: No. US2002017565A1an, Garry P.

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

APPLICANT: Hitoshi, Yasumichi

US-10-105-545-26

Query Match 36.9%; Score 486; DB 14; Length 93;  
Best Local Similarity 100.0%; Pred. No. 3e-31;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ALPAAQGNKVLGKGGDTVELTCTASQKSIQFHWKNSNOIKILGSGFLTKGPSKL 76  
DB 1 ALPAAQGNKVLGKGGDTVELTCTASQKSIQFHWKNSNOIKILGSGFLTKGPSKL 60

OTHER INFORMATION: The xaa at positions 11 through 14 represents an  
OTHER INFORMATION: unknown amino acid.  
NAME/KEY: UNSURE  
LOCATION: (28)  
OTHER INFORMATION: The xaa at position 28 represents an unknown amino  
OTHER INFORMATION: acid.  
NAME/KEY: UNSURE  
LOCATION: (41)  
OTHER INFORMATION: The xaa at position 41 represents an unknown amino  
OTHER INFORMATION: acid.  
LOCATION: (46)..(48)  
OTHER INFORMATION: The xaa at positions 46 through 48 represents an  
OTHER INFORMATION: unknown amino acid.  
NAME/KEY: UNSURE  
LOCATION: (62)  
OTHER INFORMATION: The xaa at position 62 represents an unknown amino  
OTHER INFORMATION: acid.  
US-09-135-238B-8

Query Match 25.6%; Score 337; DB 9; Length 84;  
Best Local Similarity 88.1%; Pred. No. 2e-19; 0; Indels 10; Gaps 5;  
Matches 74; Conservative 0; Mismatches 0; Indels 10; Gaps 5;

QY 37 VELICTASOK---XSIOFHMNNSNOI-KIIGNOGSFLTK-GPSK--LNDRADSRRLSLW 87  
DB 1 VELICTASOKXXXXXSIOFHMNNSNOIKIIGNOGSFLTKXGPSXXXXLNDRADSRRLSLW 60

QY 88 D-QGNFPLIKKLIKIEDSDTYICE 110  
DB 61 DQGNFPLIKKLIKIEDSDTYICE 84

RESULT 38  
US-09-997-165-2  
Sequence 2, Application US/09997165  
Patent No. US2002014199A1  
GENERAL INFORMATION:  
APPLICANT: Lyman, Stewart D.  
APPLICANT: Fanelow, William C.  
TITLE OF INVENTION: LIGAND FOR CD7 AND METHODS OF USE THEREOF  
FILE REFERENCE: 2913-US  
CURRENT APPLICATION NUMBER: US/09/997,165  
CURRENT FILING DATE: 2001-11-27  
PRIOR APPLICATION NUMBER: PCT/US00/14612  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/136,450  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 2  
LENGTH: 240  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-997-165-2

Query Match 25.2%; Score 332; DB 9; Length 240;  
Best Local Similarity 36.4%; Pred. No. 1.9e-18;  
Matches 102; Conservative 18; Mismatches 54; Indels 106; Gaps 10;

QY 6 PRRLLLVLTAL---LPAATGKNKVLGKK-----GTVELCTASOKXSIOFHMNS 56  
DB 4 PRRLLLVLTALGLPALAAQEVQSPHCTVPVGSVITCSTSG----- 52

QY 57 NQIKLNGSFLTK-GPS-----KNDRADSRRLMDQGNFPLIKN 98  
DB 53 -----GNGIYLRQIGPQPDIIYEDGVPTTDRRFRGRIDFSGS---QDNLITTPHR 103

QY 99 LKIEDSDTYICEVEDQKEEVQLVFLGTANSPTHLQSGSLTLTLESPPGSSPSVQCRSP 158  
DB 104 LQLSDTGTTC-----QATREV----- 120

QY 159 RGNIGGKTLISVSOLEIDSGTWTCTVLQNGKVEFKIDIVPRASALPAPPTGSLPDP 218

DB 121 ---NVYSGTL-VLVEEQSGWHRCS-----DAPPRASALPAPPTGSLPDP 164  
QY 219 QTASALPDPAPASALPALAVISFLGLGIGVACVLARTR 258  
DB 165 QTASALPDPAPASALPALAVISFLGLGIGVACVLARTQ 204

RESULT 39  
US-09-939-537-35  
Sequence 35, Application US/09939537  
Publication No. US20030138410A1  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian  
Banapour, Babak  
Romeo, Charles  
Kolanus, Waldemar

TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED  
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,537  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/284,391  
FILING DATE: 02-AUG-1994  
APPLICATION NUMBER: 08/195,395  
FILING DATE: 14-FEB-1994

APPLICATION NUMBER: 07/847,566  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/665,961  
FILING DATE: 07-MAR-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Elbing, Karen L.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/247001

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-939-537-35

Query Match 21.9%; Score 288; DB 10; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1e-15;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 PRASALPAPPTGSLPDPQTASALPDPAPASALPALAVISFLGLGIGVACVLARTR 258  
DB 1 PRASALPAPPTGSLPDPQTASALPDPAPASALPALAVISFLGLGIGVACVLARTR 58

RESULT 40

```
US-10-105-545-25
; Sequence 25, Application US/10105545
; Publication No. US20030144479A1
; GENERAL INFORMATION:
; APPLICANT: Mark, Greene I.
; APPLICANT: Williams, William V.
; APPLICANT: Weiner, David B.
; APPLICANT: Cohen, Jeffery A.
; APPLICANT: Kieher-Emmons, Thomas
; APPLICANT: Williams, Robert M.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND USI
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 4040/11492US2
; CURRENT APPLICATION NUMBER: US/10/105,545
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 08/752,816
; PRIOR FILING DATE: 1996-11-21
; PRIOR APPLICATION NUMBER: US 07/940,654
; PRIOR FILING DATE: 1992-09-03
; PRIOR APPLICATION NUMBER: US 07/702,833
; PRIOR FILING DATE: 1991-05-20
; PRIOR APPLICATION NUMBER: US 07/326,328
; PRIOR FILING DATE: 1989-03-21
; PRIOR APPLICATION NUMBER: US 07/074,264
; PRIOR FILING DATE: 1987-07-16
; PRIOR APPLICATION NUMBER: US 07/462,542
; PRIOR FILING DATE: 1990-01-09
; PRIOR APPLICATION NUMBER: US 07/648,303
; PRIOR FILING DATE: 1991-01-25
; PRIOR APPLICATION NUMBER: US 07/685,881
; PRIOR FILING DATE: 1991-04-15
; PRIOR APPLICATION NUMBER: US 07/574,391
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: US 07/194,026
; PRIOR FILING DATE: 1988-05-13
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-105-545-25

Query Match      18.1%; Score 238; DB 14; Length 95;
Best Local Similarity 54.3%; Pred. No. 1.8e-11;
Matches 51; Conservative 14; Mismatches 25; Indels 4; Gaps 3;

QY      19 LPAATGKRVYGGKGVLTCTASQKSIQFHWKNSQIKILNQG-SFLTKG--PSK 75
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      3 LLAVTGKTLVKGKESAELEPSSQKKITVTFWTFSDQRKILGQHGKGVLRIGGSPSQ 62

QY      76 LNDRADRSRLMDQGNFPLIINKLKTEDSDTYIC 109
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      63 F-DREDSKKGAWKGSFPLINKLKTEDSDTYIC 95

RESULT 41
US-10-076-674-4
; Sequence 4, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 50
```

```
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4

Query Match      11.4%; Score 150; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      64 NQGSFLTKGSPSKLNDRADRSRLMDQGN 91
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      22 NQGSFLTKGSPSKLNDRADRSRLMDQGN 49

RESULT 42
US-10-076-674-5
; Sequence 5, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-5

Query Match      11.4%; Score 150; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      64 NQGSFLTKGSPSKLNDRADRSRLMDQGN 91
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      22 NQGSFLTKGSPSKLNDRADRSRLMDQGN 49

RESULT 43
US-10-355-161A-4
; Sequence 4, Application US/10355161A
; Publication No. US2004009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-4

Query Match      11.4%; Score 150; DB 15; Length 50;
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Best Local Similarity 100.0%; Pred. No. 8.5e-05;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 NOGSFLTGPSTKLNDRADSRSLMDQGN 91  
DB 22 NOGSFLTGPSTKLNDRADSRSLMDQGN 49

RESULT 44  
US-10-355-161A-5

; Sequence 5, Application US/10355161A  
; Publication No. US20040009897A1  
; GENERAL INFORMATION:  
; APPLICANT: Sokoll, Kenneth K.  
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System  
; FILE REFERENCE: Immunogen Delivery System  
; CURRENT APPLICATION NUMBER: US/10/355,161A  
; PRIOR FILING DATE: 2003-01-31  
; PRIOR APPLICATION NUMBER: US 10/076674  
; PRIOR FILING DATE: 2002-02-14  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (20)\_(20)  
; OTHER INFORMATION: Xaa indicates epsilon-Lys  
US-10-355-161A-5

Query Match 11.4%; Score 150; DB 15; Length 50;  
Best Local Similarity 100.0%; Pred. No. 8.5e-05;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 NOGSFLTGPSTKLNDRADSRSLMDQGN 91  
DB 22 NOGSFLTGPSTKLNDRADSRSLMDQGN 49

RESULT 45  
US-10-311-823-13

; Sequence 13, Application US/10311823  
; Publication No. US20040116683A1  
; GENERAL INFORMATION:  
; APPLICANT: Bryan J. Boyle  
; APPLICANT: Nancy Mize  
; APPLICANT: Matthew Arterburn  
; APPLICANT: Y. Tom Tang  
; APPLICANT: George Yeung  
; APPLICANT: Ping Zhou  
; APPLICANT: Chenghua Liu  
; APPLICANT: Vinod Asundi  
; APPLICANT: Radoje T. Drmanac  
; APPLICANT: Meng-Yun Wang  
; APPLICANT: Lichuan Chen  
; APPLICANT: Yea-Huey Yang  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTROPIC-LIKE  
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: HYS-17C1P/US  
; CURRENT APPLICATION NUMBER: US/10/311,823  
; PRIOR FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: PCT/US01/03651  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/632,085  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13  
; LENGTH: 570  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-311-823-13

Query Match 10.6%; Score 139; DB 16; Length 570;  
Best Local Similarity 26.3%; Pred. No. 0.014;  
Matches 56; Conservative 33; Mismatches 82; Indels 42; Gaps 9;

QY 4 GVPFRHLIVLQALLPAATQGNKVLGKGD-----TVELTCTASQKKSIGFHWKNSQ 58  
DB 99 GVPFRHLIVLQALLPAATQGNKVLGKGD-----TVELTCTASQKKSIGFHWKNSQ 157  
QY 59 IKILNGSGFLTGPSTKLNDRADSRSLMDQGNPPLI-IRKLKTEDSDTYICEVEDQKE- 116  
DB 158 -----TSHSQDNG-VDIYEPLTYOGETKVLKRLRPQDYASTYQVSVKRV 205  
QY 117 --EVQLVFGITLANSDFHLQGGSLTTLSPSSPSVQC-----R 156  
DB 206 GIPDKAITPRLTNTTAPPAK-LSVNETLVNPGENVTVQCLTGTGDPPLPQLQWSHGPG 264  
QY 157 SPGRNIGGKTLVSQLELDSDSTWTCYVLQN 189  
DB 265 LPLGALQGG-TLSIPVQARDSGYNCATNN 296

RESULT 46  
US-10-311-823-7

; Sequence 7, Application US/10311823  
; Publication No. US20040116683A1  
; GENERAL INFORMATION:  
; APPLICANT: Bryan J. Boyle  
; APPLICANT: Nancy Mize  
; APPLICANT: Matthew Arterburn  
; APPLICANT: Y. Tom Tang  
; APPLICANT: George Yeung  
; APPLICANT: Ping Zhou  
; APPLICANT: Chenghua Liu  
; APPLICANT: Vinod Asundi  
; APPLICANT: Radoje T. Drmanac  
; APPLICANT: Meng-Yun Wang  
; APPLICANT: Lichuan Chen  
; APPLICANT: Yea-Huey Yang  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTROPIC-LIKE  
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES  
; FILE REFERENCE: HYS-17C1P/US  
; CURRENT APPLICATION NUMBER: US/10/311,823  
; PRIOR FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: PCT/US01/03651  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/632,085  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 586  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-311-823-7

Query Match 10.6%; Score 139; DB 16; Length 586;  
Best Local Similarity 26.3%; Pred. No. 0.015;  
Matches 56; Conservative 33; Mismatches 82; Indels 42; Gaps 9;

QY 4 GVPFRHLIVLQALLPAATQGNKVLGKGD-----TVELTCTASQKKSIGFHWKNSQ 58  
DB 115 GVPFRHLIVLQALLPAATQGNKVLGKGD-----TVELTCTASQKKSIGFHWKNSQ 173





```

RESULT 50
US-10-211-462-87
; Sequence 87, Application US/10211462
; Publication No. US2004003495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natsheh
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 87
; LENGTH: 1496
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-87

Query Match          10.0%; Score 131.5; DB 12; Length 1496;
Best Local Similarity 26.5%; Pred. No. 0.19; Indels 47; Gaps 9;
Matches 60; Conservative 27; Mismatches 92;

Qy 34 GDTVELTCTASQKSIQFHMKNSTQIKILNGSGFLTKPSKLNDRADSRSLMDQGNFP 93
Db 277 GNTVFTCTAGNPKPEIIMLRNN-----NLSMKTKDSRLNLLDDGT-- 318
Qy 94 LIINKLKIEDSDTYICEV-----EDQKEEVLVFGLTAN-----SDTHLLQGQSILTL 141
Db 319 LMIONTOETDQGIYQCAKNAVAGEVKTQEVTLRYFGSPARPTFVIOPTQTEVLVGESEVTL 378
Qy 142 -----TLSPSSPSVQCRSP-----RGKNIQGGKTLVSQLELDQSGTWTCTVLONOKV 193
Db 379 ECSATGHPPTISWTRGDRTPLPVDRVNIPTSGGLYIQNVQSGSEYACSATNNIDSV 438
Qy 194 EFKIDIVPRASALP---APPTGSALPDPQT---ASALPDPAPASA 232
Db 439 HATAFII--VQALLPQFTVTPQDRVIVIEGQTVDFQCEAKGNPPVIA 482

RESULT 51
US-10-021-660-125
; Sequence 125, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/10/021,660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11

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```

; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 125
; LENGTH: 1496
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-021-660-125

Query Match          10.0%; Score 131.5; DB 14; Length 1496;
Best Local Similarity 26.5%; Pred. No. 0.19; Indels 47; Gaps 9;
Matches 60; Conservative 27; Mismatches 92;

Qy 34 GDTVELTCTASQKSIQFHMKNSTQIKILNGSGFLTKPSKLNDRADSRSLMDQGNFP 93
Db 277 GNTVFTCTAGNPKPEIIMLRNN-----NLSMKTKDSRLNLLDDGT-- 318
Qy 94 LIINKLKIEDSDTYICEV-----EDQKEEVLVFGLTAN-----SDTHLLQGQSILTL 141
Db 319 LMIONTOETDQGIYQCAKNAVAGEVKTQEVTLRYFGSPARPTFVIOPTQTEVLVGESEVTL 378
Qy 142 -----TLSPSSPSVQCRSP-----RGKNIQGGKTLVSQLELDQSGTWTCTVLONOKV 193
Db 379 ECSATGHPPTISWTRGDRTPLPVDRVNIPTSGGLYIQNVQSGSEYACSATNNIDSV 438
Qy 194 EFKIDIVPRASALP---APPTGSALPDPQT---ASALPDPAPASA 232
Db 439 HATAFII--VQALLPQFTVTPQDRVIVIEGQTVDFQCEAKGNPPVIA 482

RESULT 52
US-10-331-496A-28
; Sequence 28, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ, GRETCHEN
; APPLICANT: HILLAN, KENNETH J.
; APPLICANT: PHILLIPS, HEIDI S.
; APPLICANT: POLAKIS, PAUL
; APPLICANT: SMITH, VICTORIA
; APPLICANT: SPENCER, SUSAN D.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WU, THOMAS D.
; APPLICANT: ZHANG, ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5014R1-PCT
; CURRENT APPLICATION NUMBER: US/10/331,496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 28
; LENGTH: 1496
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-331-496A-28

```

[illegible]

```

APPLICANT: Meng, Gezhi
APPLICANT: Ma, Yundong
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 807A
CURRENT APPLICATION NUMBER: US//10/243,552
CURRENT FILING DATE: 2002-09-12
PRIORITY APPLICATION NUMBER: US 60/332,511
PRIORITY FILING DATE: 2001-09-13
PRIORITY APPLICATION NUMBER: PCT/US00/35017
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US 09/488,725
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: US 09/552,317
PRIORITY FILING DATE: 2000-04-25
PRIORITY APPLICATION NUMBER: PCT/US01/02623
PRIORITY FILING DATE: 2001-01-25
PRIORITY APPLICATION NUMBER: US 09/491,404
PRIORITY FILING DATE: 2000-01-25
PRIORITY APPLICATION NUMBER: PCT/US01/03600
PRIORITY FILING DATE: 2001-02-05
PRIORITY APPLICATION NUMBER: US 09/496,914
PRIORITY FILING DATE: 2000-02-03
PRIORITY APPLICATION NUMBER: US 09/560,875
PRIORITY FILING DATE: 2000-04-27
PRIORITY APPLICATION NUMBER: PCT/US01/04927
PRIORITY FILING DATE: 2001-02-26
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 998
SOFTWARE: pt_fl_genes Version 5.0
SEQ ID NO 899
LENGTH: 1498
TYPE: PRT
ORGANISM: Homo sapiens
US-10-243-552-899

Query Match      10.0%; Score 131.5; DB 12; Length 1498;
Best Local Similarity 26.5%; Pred. No. 0.19;
Matches 60; Conservative 27; Mismatches 92; Indels 47; Gaps 9;

Oy 34 GDVTELCTSSQKKSIOFHMNSNQIKILNQGSFLTKGPEKINDRADSRSLWDQGNFP 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 277 GNTVYFCRABGNKPELIMLRN-----NELSMKTDLSRLNLDGCT-- 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 94 LIINKLEIEDSDYICEV-----EDQKEVQLVFGILTAN-----SDTHLLQGQSITL 141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 LMIGNQETQGLIQCAKAVAGVGTQKEVTLRFSGPARPTFVIQONTPEVLVGESVTL 376
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 142 ---TLESPPGSSPVQCRSP---RGKNIOGKTLVSQLELSDSGTWTCTVLOAQKV 193
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 ECSATGHPPIRISWTRDRTFLPVDPRVNIITPSGGLYIONVQDSEGYACSATNIDSV 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 194 EFKIDIVPRASALP---APPTGSALPPPQT---ASALPPPRASA 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 HATAFII-VQALPQFTVTPODRVIVIEGQIVDFQCEAKGNPPVIA 482
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 55
US-10-311-823-16
; Sequence 16, Application US/10311823
; Publication No. US20040116683A1
; GENERAL INFORMATION:
; APPLICANT: Bryan J. Boyle
; APPLICANT: Nancy Mize
; APPLICANT: Matthew Arterburn
; APPLICANT: Y. Tom Tang
; APPLICANT: George Yeung
; APPLICANT: Ping Zhou
; APPLICANT: Chenghua Liu
; APPLICANT: Vinod Asundi
; APPLICANT: Radoje T. Drmanac
; APPLICANT: Weng-Yun Wang
; APPLICANT: Lichuan Chen

```

```

; APPLICANT: Yea-Huey Yang
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTROPIC-LIKE
; FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: HYS-17CIP/US
; CURRENT APPLICATION NUMBER: US/10/311,823
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/US01/03651
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/632,085
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-311-823-16

Query Match          9.9%; Score 131; DB 16; Length 374;
Best Local Similarity 27.3%; Pred. No. 0.036;
Matches 48; Conservative 25; Mismatches 67; Indels 36; Gaps 7;

QY 36 TVELCTASQKKSIOFHKNSNQIKLGNQSFITKPSKNDADRSRLMDQGNFPLI 95
DB 55 TVFLRCTVNSNPAPRFTWKRGSD-----TLSHSDNG-VDIYEPLYTGSETKVL 102
QY 96 -IKNLKIEDSDPTYICEVEDQK---EVQLVFGLTANSPTHLQGSLLTLIESPGSSP 151
DB 103 KLNLRPDYASVYTCQSVRVNCGIPDKAITFRLTNTTAPPAK-LSVNETLVNPGENV 161
QY 152 SVQC-----RSPRGKNIQGGKTLVSQLELDSDGTWCTVION 189
DB 162 TVQCLLTGSDPLPOLQWSHGPGPLPLGALAQGG-TLSIPSVQARDSGVYNCTATNN 216

RESULT 56
US-10-311-823-12
; Sequence 12, Application US/10311823
; Publication No. US20040116683A1
; GENERAL INFORMATION:
; APPLICANT: Bryan J. Boyle
; APPLICANT: Nancy Mize
; APPLICANT: Matthew Arterburn
; APPLICANT: Y. Tom Tang
; APPLICANT: George Yeung
; APPLICANT: Ping Zhou
; APPLICANT: Chenghua Liu
; APPLICANT: Vinod Asundi
; APPLICANT: Radoje T. Drmanac
; APPLICANT: Meng-Yun Wang
; APPLICANT: Yea-Huey Yang
; APPLICANT: Lichuan Chen
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTROPIC-LIKE
; FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: HYS-17CIP/US
; CURRENT APPLICATION NUMBER: US/10/311,823
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/US01/03651
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/632,085
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 442
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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-311-823-12

Query Match          9.9%; Score 131; DB 16; Length 442;
Best Local Similarity 27.3%; Pred. No. 0.044;
Matches 48; Conservative 25; Mismatches 67; Indels 36; Gaps 7;

QY 36 TVELCTASQKKSIOFHKNSNQIKLGNQSFITKPSKNDADRSRLMDQGNFPLI 95
DB 136 TVFLRCTVNSNPAPRFTWKRGSD-----TLSHSDNG-VDIYEPLYTGSETKVL 183
QY 96 -IKNLKIEDSDPTYICEVEDQK---EVQLVFGLTANSPTHLQGSLLTLIESPGSSP 151
DB 184 KLNLRPDYASVYTCQSVRVNCGIPDKAITFRLTNTTAPPAK-LSVNETLVNPGENV 242
QY 152 SVQC-----RSPRGKNIQGGKTLVSQLELDSDGTWCTVION 189
DB 243 TVQCLLTGSDPLPOLQWSHGPGPLPLGALAQGG-TLSIPSVQARDSGVYNCTATNN 297

RESULT 57
US-10-311-823-4
; Sequence 4, Application US/10311823
; Publication No. US20040116683A1
; GENERAL INFORMATION:
; APPLICANT: Bryan J. Boyle
; APPLICANT: Nancy Mize
; APPLICANT: Matthew Arterburn
; APPLICANT: Y. Tom Tang
; APPLICANT: George Yeung
; APPLICANT: Ping Zhou
; APPLICANT: Chenghua Liu
; APPLICANT: Vinod Asundi
; APPLICANT: Radoje T. Drmanac
; APPLICANT: Meng-Yun Wang
; APPLICANT: Lichuan Chen
; APPLICANT: Yea-Huey Yang
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTROPIC-LIKE
; FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: HYS-17CIP/US
; CURRENT APPLICATION NUMBER: US/10/311,823
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/US01/03651
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/632,085
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-311-823-4

Query Match          9.9%; Score 131; DB 16; Length 458;
Best Local Similarity 27.3%; Pred. No. 0.046;
Matches 48; Conservative 25; Mismatches 67; Indels 36; Gaps 7;

QY 36 TVELCTASQKKSIOFHKNSNQIKLGNQSFITKPSKNDADRSRLMDQGNFPLI 95
DB 152 TVFLRCTVNSNPAPRFTWKRGSD-----TLSHSDNG-VDIYEPLYTGSETKVL 199
QY 96 -IKNLKIEDSDPTYICEVEDQK---EVQLVFGLTANSPTHLQGSLLTLIESPGSSP 151
DB 200 KLNLRPDYASVYTCQSVRVNCGIPDKAITFRLTNTTAPPAK-LSVNETLVNPGENV 258
QY 152 SVQC-----RSPRGKNIQGGKTLVSQLELDSDGTWCTVION 189
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Db 259 TVQCLLTGDDPLPQLQWHSHPGLPLGALAGG-TLISIPVQARDSGVYNCTATNN 313

RESULT 58

US-10-024-918-27

/ Sequence 27, Application US/10024918

/ Publication No. US20020168718A1

/ GENERAL INFORMATION:

/ APPLICANT: Hubbell, Jeffrey

/ APPLICANT: Schenck, Jason

/ APPLICANT: Zisch, Andreas

/ APPLICANT: Hall, Heike

/ TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING

/ FILE REFERENCE: CIT 2606 CIP

/ CURRENT APPLICATION NUMBER: US/10/024,918

/ CURRENT FILING DATE: 2001-12-18

/ NUMBER OF SEQ ID NOS: 33

/ SOFTWARE: Patentin version 3.1

/ SEQ ID NO 27

/ LENGTH: 1260

/ TYPE: PRT

/ ORGANISM: Mus Musculus

/ FEATURE:

/ NAME/KEY: MISC FEATURE

/ LOCATION: (516)..(604)

/ OTHER INFORMATION: the sixth Ig-1-like domain of the cell adhesion molecule L1

US-10-024-918-27

Query Match 9.9%; Score 131; DB 13; Length 1260;

Best Local Similarity 23.9%; Pred. No. 0.17;

Matches 56; Conservative 33; Mismatches 95; Indels 50; Gaps 9;

Qy 10 LLLVLQALLPAAQGNKVVGLGKGDVTELTCTASQKSIQ--FHWKNSNQKILGNQGS 67

Db 507 ILANLQVKEATQTTCQPSAIEKKGARVFTCOASDPQLQASTIRWGDGR----- 557

Qy 68 FLTGPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYIC---EVEDQKEVQLLVF 123

Db 558 -----DLQERGDSDKXFIEDGK--LVIGSLDYSQGNYSQVASTELDEVESRAQLLV 608

Qy 124 GLTAN-----SDTHLQGSITLTLESPPGSSPSVQCRRP-----RGKNIQGGKTL 169

Db 609 GSPGPVPHLELSDRHLKQSQVHLSSW-----SPAEDHNSPIEKYDIEFEDKEMAPEKWF 662

Qy 170 SVSQLELDQSGTWCTCTVLQNGKVE--FKIDIVPRASALPAPPTGSALPDPOTA 221

Db 663 SLGKV----PGNQSTTLKLSPIVHYTFRTAINKYGPSPVSESVVTPPEAA 712

RESULT 59

US-10-650-509-27

/ Sequence 27, Application US/10650509

/ Publication No. US20040082513A1

/ GENERAL INFORMATION:

/ APPLICANT: Hubbell, Jeffrey

/ APPLICANT: Schenck, Jason

/ APPLICANT: Zisch, Andreas

/ APPLICANT: Hall, Heike

/ TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING

/ FILE REFERENCE: CIT 2606 CIP CON

/ CURRENT APPLICATION NUMBER: US/10/650,509

/ CURRENT FILING DATE: 2003-08-27

/ PRIOR APPLICATION NUMBER: 10/024,918

/ PRIOR FILING DATE: 2001-12-18

/ PRIOR APPLICATION NUMBER: 09/057,052

/ PRIOR FILING DATE: 1998-04-08

/ PRIOR APPLICATION NUMBER: PCT/US99/06617

/ PRIOR FILING DATE: 1998-04-02

/ PRIOR APPLICATION NUMBER: 60/042,143

/ PRIOR FILING DATE: 1997-04-03

/ NUMBER OF SEQ ID NOS: 33

/ SOFTWARE: Patentin version 3.1

/ SEQ ID NO 27

/ LENGTH: 1260

/ TYPE: PRT

/ ORGANISM: Mus Musculus

/ FEATURE:

/ NAME/KEY: MISC FEATURE

/ LOCATION: (516)..(604)

/ OTHER INFORMATION: the sixth Ig-1-like domain of the cell adhesion molecule L1

US-10-650-509-27

Query Match 9.9%; Score 131; DB 16; Length 1260;

Best Local Similarity 23.9%; Pred. No. 0.17;

Matches 56; Conservative 33; Mismatches 95; Indels 50; Gaps 9;

Qy 10 LLLVLQALLPAAQGNKVVGLGKGDVTELTCTASQKSIQ--FHWKNSNQKILGNQGS 67

Db 507 ILANLQVKEATQTTCQPSAIEKKGARVFTCOASDPQLQASTIRWGDGR----- 557

Qy 68 FLTGPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYIC---EVEDQKEVQLLVF 123

Db 558 -----DLQERGDSDKXFIEDGK--LVIGSLDYSQGNYSQVASTELDEVESRAQLLV 608

Qy 124 GLTAN-----SDTHLQGSITLTLESPPGSSPSVQCRRP-----RGKNIQGGKTL 169

Db 609 GSPGPVPHLELSDRHLKQSQVHLSSW-----SPAEDHNSPIEKYDIEFEDKEMAPEKWF 662

Qy 170 SVSQLELDQSGTWCTCTVLQNGKVE--FKIDIVPRASALPAPPTGSALPDPOTA 221

Db 663 SLGKV----PGNQSTTLKLSPIVHYTFRTAINKYGPSPVSESVVTPPEAA 712

RESULT 60

US-10-094-886-52

/ Sequence 52, Application US/10094886

/ Publication No. US2004002120A1

/ GENERAL INFORMATION:

/ APPLICANT: Kekuda, Ramesh

/ APPLICANT: Tcherny, Velizar T.

/ APPLICANT: Liu, Xiaohong

/ APPLICANT: Spytek, Kimberly A.

/ APPLICANT: Patturajan, Meera

/ APPLICANT: Burgess, Catherine

/ APPLICANT: Vernet, Corine A.

/ APPLICANT: Li, Li

/ APPLICANT: Gorman, Linda

/ APPLICANT: Malyankar, Uriel M.

/ APPLICANT: Boldog, Ferenc

/ APPLICANT: Guo, Xiaojia

/ APPLICANT: Shenoy, Suresh

/ APPLICANT: Padigaru, Muralidhara

/ APPLICANT: Taupier, Raymond J., Jr.

/ APPLICANT: Miller, Charles

/ APPLICANT: Casman, Stacie

/ APPLICANT: Pena, Carol

/ APPLICANT: Gangoli, Bsha

/ APPLICANT: Gusev, Vladimir

/ APPLICANT: Smithson, Glenda

/ APPLICANT: Zernusen, Bryan

/ APPLICANT: Gerlach, Valerie

/ APPLICANT: Pochart, Pascal

/ APPLICANT: Fernandes, Blma

/ APPLICANT: Shinkets, Richard

/ APPLICANT: Raestelli, Luca

/ APPLICANT: Spaderma, Steven

/ APPLICANT: Larochele, William

/ APPLICANT: Zhong, Mei

/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

/ FILE REFERENCE: 21402-290 B

/ CURRENT APPLICATION NUMBER: US/10/094,886

/ CURRENT FILING DATE: 2002-03-07

/ PRIOR APPLICATION NUMBER: 60/274,322

/ PRIOR FILING DATE: 2001-03-08

/ PRIOR APPLICATION NUMBER: 60/313,182

/ PRIOR FILING DATE: 2001-08-17

```

P R I O R   A P P L I C A T I O N   N U M B E R :   60 / 288 , 052
P R I O R   F I L I N G   D A T E :   2001-05-02
P R I O R   A P P L I C A T I O N   N U M B E R :   60 / 318 , 510
P R I O R   F I L I N G   D A T E :   2001-09-10
P R I O R   A P P L I C A T I O N   N U M B E R :   60 / 274 , 281
P R I O R   F I L I N G   D A T E :   2001-03-08
P R I O R   A P P L I C A T I O N   N U M B E R :   60 / 314 , 018
P R I O R   F I L I N G   D A T E :   2001-08-21
P R I O R   A P P L I C A T I O N   N U M B E R :   60 / 274 , 194
P R I O R   F I L I N G   D A T E :   2001-03-08
P R I O R   A P P L I C A T I O N   N U M B E R :   60 / 274 , 849
P R I O R   F I L I N G   D A T E :   2001-03-09
P R I O R   A P P L I C A T I O N   N U M B E R :   60 / 296 , 693
P R I O R   F I L I N G   D A T E :   2001-06-07
P R I O R   A P P L I C A T I O N   N U M B E R :   60 / 313 , 626
P R I O R   F I L I N G   D A T E :   2001-08-21
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 298
SOFTWARE: PatentIn 2.1
SEQ ID NO 52
LENGTH: 1315
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-886-52

Query Match      9.9%; Score 131; DB 15; Length 1315;
Best Local Similarity 27.3%; Pred. No. 0.18;
Matches 48; Conservative 25; Mismatches 67; Indels 36; Gaps 7;

Cy 36 TVELTCTSAQKKSIIOFHKNKSNQIILNQGSEFLTKGPKSKLNDRADSRSLMDQGNFPLI 95
Db 152 TVFAKCTVNSPPAPAFIMKRGGD-----TLSSHQDNG-VDIYEPLYTGETKYVL 199
Cy 96 -IKNLKIEDSDPYLYICEVEDOKE---EVQLLVFGLTANSDDTHLLQGQSITLLTESPGSSP 151
Db 200 KLNKLRPDPDYASTYQTQGVSVRNVCGIPDKAITFRLLNTTAAPRLK-LSVNETILVYVNGENV 258
Cy 152 SVQC-----RSPRGKNIGCKGLTSVSQLELDQSGTWCTTVLON 189
Db 259 TVQCILTTGDDPLPOLQWMSHGPGPLDLGALLAQGG-TLSIPVSQARDSGYNNCTATANN 313

RESULT 61
US-10-094-886-38
Sequence 38, Application US/10094886
Publication No. US20040002120A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Tcherneny, Velizar T.
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patuturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Vernet, Corine A.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Malysankar, Uriel M.
APPLICANT: Boldog, Ferenc
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh
APPLICANT: Padigaru, Muralihara
APPLICANT: Taupier, Raymond J., Jr.
APPLICANT: Miller, Charles
APPLICANT: Casman, Stacie
APPLICANT: Pena, Carol
APPLICANT: Gangoli, Beba
APPLICANT: Gusev, Vladimir
APPLICANT: Smithson, Glenda
APPLICANT: Zethusen, Bryan
APPLICANT: Gerlach, Valerie
APPLICANT: Pochart, Pascal
APPLICANT: Fernandes, Elma
APPLICANT: Shimkets, Richard

```

```

; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Larocheille, William
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD-
; FILE REFERENCE: 21402-290 B
; CURRENT APPLICATION NUMBER: US/10/094,886
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,182
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/288,052
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/318,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/314,018
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/296,693
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/313,626
; PRIOR FILING DATE: 2001-08-21
; Remaining Prior Application data removed - see file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 38
; LENGTH: 1386
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-886-38

Query Match      9.9%; Score 131; DB 15; Length 1386;
Beat Local Similarity 27.3%; Pred. No. 0.19;
Matches 48; Conservative 25; Mismatches 67; Indels 36; Gaps 7;

QY      36 TVELTCTSAQSOKSIGIFHMKNSNQIKILNQGSLFTKGPSTKLNRADRSRLMDGNEPLI 95
DB      152 TVFNFCTVSNNDPAPFIWGRGSD-----TLSHSQDNG-VDIYEPLYTGSETKVL 199
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      96 -IKNLKIEDSDTYICEVEDOKE---EVQLIVFGLTANSDTHLHQGSILFTLESPPGSSP 151
          :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB      200 KLNKLRPDQYASYTCQVSVRANGCIPDKAITPRLLTNTYTAPPALK-LSVNETLVVNPGENV 258
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      152 SVQC-----RSPRGKNIIQGGKITLSVSQLDLQDSGTWTCTVIQN 189
          :||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      259 TVQCULTGTGDPLPQLQWSHGPGPLPIGLALAGG-TLSIPVGARDSDGYNCTATNN 313

RESULT 62
US-09-808-602-69
; Sequence 69, Application US/09808602
; Patent No. US2002015515A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US2002015515A1 Proteins and Nuclec Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05

```

```

; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-69

Query Match
Best Local Similarity 23.2%; Score 129; DB 9; Length 338;
Matches 57; Conservative 40; Mismatches 91; Indels 58; Gaps 11;

QY 10 LLLVQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIOFHKNNSQIKI 61
   ||:|||||
DB 14 LVLLRLCLLPGLPVRSDVFNKGTNITVRQGDFAILRCVLEDKNS-KVAMLNNSGILIF 72
   ||:|||||

QY 62 LQNGSFLTKGSPSKLNDRA--DSRRSLMDQGNPFLIKIKLIKEDSDTYICEVEDQKE--- 116
   ||:|||||
DB 73 AGHD-----KMSLDPRVLELKRHSL---EYSLRIQKVDVDEGSYTCVSQTQHEPKT 121
   ||:|||||

QY 117 -EVQLVFG---LTANSDTHLQGSILTLLESPPGSSPSVQCR--SPRGKNIQSGKT- 168
   ||:|||||
DB 122 SQVYLIVQVPPKISNISDVTVNEGSNVTLVCMANGRPPEPVITWHLPTGREFGESEY 181
   ||:|||||

QY 169 LSVSLELDSDGTWTCTVLIQ-----NOKKVEFKIDIVP-----RA 203
   ||:|||||
DB 182 LEILGITREQSGKYCKAKANEVSADVKQVTVNYPPTITBSKSNATTTGRQSLKCEA 241
   ||:|||||

QY 204 SALPAP 209
   ||:|||||
DB 242 SAVPAP 247

RESULT 63
US-09-800-198-58
; Sequence 58, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkens, Richard A
; APPLICANT: Herrmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Raschell, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-198-58

Query Match
Best Local Similarity 9.8%; Score 129; DB 10; Length 338;
Matches 57; Conservative 40; Mismatches 91; Indels 58; Gaps 11;

QY 10 LLLVQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIOFHKNNSQIKI 61
   ||:|||||
DB 14 LVLLRLCLLPGLPVRSDVFNKGTNITVRQGDFAILRCVLEDKNS-KVAMLNNSGILIF 72
   ||:|||||

QY 62 LQNGSFLTKGSPSKLNDRA--DSRRSLMDQGNPFLIKIKLIKEDSDTYICEVEDQKE--- 116
   ||:|||||
DB 73 AGHD-----KMSLDPRVLELKRHSL---EYSLRIQKVDVDEGSYTCVSQTQHEPKT 121
   ||:|||||
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QY 117 -EVQLVFG---LTANSDTHLQGSILTLLESPPGSSPSVQCR--SPRGKNIQSGKT- 168
   ||:|||||
DB 122 SQVYLIVQVPPKISNISDVTVNEGSNVTLVCMANGRPPEPVITWHLPTGREFGESEY 181
   ||:|||||

QY 169 LSVSLELDSDGTWTCTVLIQ-----NOKKVEFKIDIVP-----RA 203
   ||:|||||
DB 182 LEILGITREQSGKYCKAKANEVSADVKQVTVNYPPTITBSKSNATTTGRQSLKCEA 241
   ||:|||||

QY 204 SALPAP 209
   ||:|||||
DB 242 SAVPAP 247

RESULT 64
US-10-042-865-92
; Sequence 92, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spyrek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esna A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Miller, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-865-92

Query Match
Best Local Similarity 9.8%; Score 129; DB 12; Length 338;
Matches 57; Conservative 40; Mismatches 91; Indels 58; Gaps 11;
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```

Db      14 LVLVLGLLCLPTGLPRVSDVFNRTGDNITVRQGDITALLRCVLEDKNS-KVAMLNRSGLIF 72
Qy      62 LQNGSFLTKGPSKLNDR--DSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQK--- 116
Db      73 AGHD-----KWSLDPVLEKRNHSL-----EYSLRIQKVADVDEGSYCSVQTOHEPKT 121
Qy      117 -EVQLLVFG---LTANSPTHLQGSLLTLESPPGSSPSVQCR--SPRGKNIQSGKT- 168
Db      122 SQVYLIVQVPKXISNISSDVTNVEGSAVTLVCMANGREPEVITWRLTPTLGRFEGEEY 181
Qy      169 LSVSOLELDQSGTWCTCTVQ-----NOKVPEFKIDIVP-----RA 203
Db      182 LEILGITRQSGKYECKKANEVSSADVQKVTVNVPPTITTSKSNKNEATTGRQASLKCEA 241
Qy      204 SALPAP 209
Db      242 SAVPAP 247

```

```

RESULT 67
US-09-808-602-72
; Sequence 72, Application US/09808602
; Patent No. US2002015515A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Hejerman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US2002015515A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-808-602-72

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Query Match      9.6%; Score 126; DB 9; Length 338;
Best Local Similarity 22.8%; Pred. No. 0.079;
Matches 56; Conservative 41; Mismatches 91; Indels 58; Gaps 11;

Qy      10 LVLVLGLLCLPAA-----TQGNKVVLGKKGDTVELTCTASQKSIQFHKNSNQIKI 61
Db      14 LVLRLCLLPGLPRLPRSDVFNRTGDNITVRQGDITALLRCVLEDKNS-KVAMLNRSGLIF 72
Qy      62 LQNGSFLTKGPSKLNDR--DSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQK--- 116
Db      73 AGHD-----KWSLDPVLEKRNHSL-----EYSLRIQKVADVDEGSYCSVQTOHEPKT 121
Qy      117 -EVQLLVFG---LTANSPTHLQGSLLTLESPPGSSPSVQCR--SPRGKNIQSGKT- 168
Db      122 SQVYLIVQVPKXISNISSDVTNVEGSAVTLVCMANGREPEVITWRLTPTLGRFEGEEY 181
Qy      169 LSVSOLELDQSGTWCTCTVQ-----NOKVPEFKIDIVP-----RA 203
Db      182 LEILGITRQSGKYECKKANEVSSADVQKVTVNVPPTITTSKSNKNEATTGRQASLKCEA 241
Qy      204 SALPAP 209
Db      242 SAVPAP 247

```

```

RESULT 68
US-09-800-198-61
; Sequence 61, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Hejerman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-800-198-61

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Query Match      9.6%; Score 126; DB 10; Length 338;
Best Local Similarity 22.8%; Pred. No. 0.079;
Matches 56; Conservative 41; Mismatches 91; Indels 58; Gaps 11;

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Qy      10 LVLVLGLLCLPAA-----TQGNKVVLGKKGDTVELTCTASQKSIQFHKNSNQIKI 61
Db      14 LVLRLCLLPGLPRLPRSDVFNRTGDNITVRQGDITALLRCVLEDKNS-KVAMLNRSGLIF 72
Qy      62 LQNGSFLTKGPSKLNDR--DSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQK--- 116
Db      73 AGHD-----KWSLDPVLEKRNHSL-----EYSLRIQKVADVDEGSYCSVQTOHEPKT 121
Qy      117 -EVQLLVFG---LTANSPTHLQGSLLTLESPPGSSPSVQCR--SPRGKNIQSGKT- 168
Db      122 SQVYLIVQVPKXISNISSDVTNVEGSAVTLVCMANGREPEVITWRLTPTLGRFEGEEY 181
Qy      169 LSVSOLELDQSGTWCTCTVQ-----NOKVPEFKIDIVP-----RA 203
Db      182 LEILGITRQSGKYECKKANEVSSADVQKVTVNVPPTITTSKSNKNEATTGRQASLKCEA 241
Qy      204 SALPAP 209
Db      242 SAVPAP 247

RESULT 69
US-10-042-865-91
; Sequence 91, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zehrusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Bsha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Paturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia

```

```

/ APPLICANT: Boldog, Ference L
/ APPLICANT: Grosse, William M
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Gerlach, Valerie L
/ APPLICANT: Edinger, Shlomit R
/ APPLICANT: Rothenberg, Mark E
/ APPLICANT: Ellerman, Karen
/ APPLICANT: MacDougall, John
/ APPLICANT: Malyankar, Uriel M
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Peyman, John
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Gunther, Erik
/ APPLICANT: Stone, David
/ TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
/ FILE REFERENCE: 21402-537
/ CURRENT APPLICATION NUMBER: US/10/042,865
/ PRIOR FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: 60/260,417
/ PRIOR FILING DATE: 2001-01-09
/ PRIOR APPLICATION NUMBER: 60/260,831
/ PRIOR FILING DATE: 2001-01-10
/ PRIOR APPLICATION NUMBER: 60/272,338
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: 60/274,876
/ PRIOR FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 60/284,704
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 264
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 91
/ LENGTH: 338
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-10-042-865-91

```

```

Query Match          9.6%; Score 126; DB 12; Length 338;
Best Local Similarity 22.8%; Pred. No. 0.079;
Matches 56; Conservative 41; Mismatches 91; Indels 58; Gaps 11;

QY 10 LLLVQLALLPRA-----TQGNKVVLGKKGDIVELCTASQKKSIOFHKNSNQIKI 61
DB 14 LVLRLRLCLPTGLPVRVSDFNRTGDMITVRQGDALRCVVEDKNS-KVAALNRSGLTF 72
QY 62 LQNGSFLTKGSPKLNDR--DSRSLMDQGNFPLIKLIKIEDSDTYICEVEDQK--- 116
DB 73 AGHD-----KMSLDPRVELEKRAL---EYSLRIQVNDVYDEGSYTCVQTOHEKXT 121
QY 117 -EVQLLVFG---LTANSPTHLLOQSLLTLLSPPGSSPSVQCR--SPRGNIIQGGKT- 168
DB 122 SQVYLIVQVPKISINSSDVTNENGSNVTLCMANGRPPEVITWRHLFPLGRFGESEBY 181
QY 169 LSVQLELQDSGTWCTVQ-----NOKKVEFKIDIV-----RA 203
DB 182 LELIGTRGSKYECKANEVSADVQKVTVNVPPTITKSKNEATITGRQASLKCEA 241
QY 204 SALPAP 209
DB 242 SAVPAP 247

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RESULT 70
US-10-042-865-14
/ Sequence 14, Application US/10042865
/ Publication No. US20040029216A1
/ GENERAL INFORMATION:
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Li, Li
/ APPLICANT: Zehusen, Bryan D
/ APPLICANT: Casman, Stacie J
/ APPLICANT: Shenoy, Suresh G
/ APPLICANT: Spytek, Kimberly

```

```

/ APPLICANT: Zhong, Mei
/ APPLICANT: Gangoli, Esha A
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Vernet, Corine A.M
/ APPLICANT: Taylor, Sarah
/ APPLICANT: Tchervnev, Velizar T
/ APPLICANT: Miller, Charles E
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Boldog, Ference L
/ APPLICANT: Grosse, William M
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Gerlach, Valerie L
/ APPLICANT: Edinger, Shlomit R
/ APPLICANT: Rothenberg, Mark E
/ APPLICANT: Ellerman, Karen
/ APPLICANT: MacDougall, John
/ APPLICANT: Malyankar, Uriel M
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Peyman, John
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Gunther, Erik
/ APPLICANT: Stone, David
/ TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
/ FILE REFERENCE: 21402-537
/ CURRENT APPLICATION NUMBER: US/10/042,865
/ PRIOR FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: 60/260,417
/ PRIOR FILING DATE: 2001-01-09
/ PRIOR APPLICATION NUMBER: 60/260,831
/ PRIOR FILING DATE: 2001-01-10
/ PRIOR APPLICATION NUMBER: 60/272,338
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: 60/274,876
/ PRIOR FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 60/284,704
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 264
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 354
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-042-865-14

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Query Match          9.6%; Score 126; DB 12; Length 354;
Best Local Similarity 23.0%; Pred. No. 0.083;
Matches 53; Conservative 37; Mismatches 92; Indels 48; Gaps 10;

QY 20 PAATQGNKVVLGKKGDIVELCTASQKKSIOFHKNSNQIKILQNGSFLTKGP-----SK 75
DB 41 PMAVDNMNV--RKGDTADRLCYLEDGAS--KGAMLNSSITFAG--GDKMSVDPRVLSIT 95
QY 76 LNDPADRSRLMDQGNFPLIKLIKIEDSDTYICEVEDQKEVOLVFGTLTA----- 127
DB 96 LNKR-----DVSLOIQVNDVYDDGPTCSVQTOHTPRMQVH-LTVQVPRXIYD 143
QY 128 -NSDPTHLLOQSLLTLLSPPGSSPSVQCR--SPRGNIIQGGKTLSSVQLELQDSGTWCT 164
DB 144 ISNDMTVNEGTNVTLLCLATGKPEPSISWRHISPAKPFENGQGLDITGTRDQAGEYEC 203
QY 185 TV-----LQNKKVEFKIDIVPRASALPAPT-----GSALPDP 218
DB 204 SAENDVSPDVRAKVKVYNFAPFTIQEIKSGVYTPGRSGILRCBAGVPPPP 253

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RESULT 71
US-09-989-722-517
/ Sequence 517, Application US/09989722
/ Patent No. US20020072067A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.

```

APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
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PRIOR FILING DATE: 1998-06-04  
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PRIOR FILING DATE: 1998-06-04  
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PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
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PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
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PRIOR FILING DATE: 1998-06-11  
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PRIOR FILING DATE: 1998-06-16  
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
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PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
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PRIOR APPLICATION NUMBER: 60/090349  
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PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24

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/ PRIOR APPLICATION NUMBER: 60/090435
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090444
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090445
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090472
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090535
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090540
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090542
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090676
/ PRIOR FILING DATE: 1998-06-25
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/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090690
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090694
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090695
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090696
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: 60/090862
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: 60/090863
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: 60/091360
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091478
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091544
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091519
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091626
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091633
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091978
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match      9.5%; Score 125; DB 9; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RHLLVLQALLPAA-ATGKNKVVAGKKDYTELTCTASQK-KSIQFMKNSNQIKLGN 64
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 2 RLVLVLMGGLLPGLVYALGPEISGFEGDVTSLQCTYAEELDRHKVYCRGGLFNSRC 61
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 65 QGSFLL-KGPSKLDRA--DSRNSLMQGNFPLIKLKLESDTYICEVEDQKEEYQ 119
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 62 SGTVAEERGQETMKGRVSRISROEL---SLIVTLWLTLDAGEYWCVEKKGPDSS 117
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 120 LLVFGLTANSDFHLLQGGSLTLTLBSPPGSSPVQCRSRKNGIKGGKTLVSOLE---- 175
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 118 LLI-----SLVFPPGPC-----CPSPSPPTFO-----PLATTRLQPPKAK 151
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 176 -----LDSGTWTCTVLQNGKVEFKIDIVPRASAL-----PA--PPT 211
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 152 AAOOTPPGLTSPGLVPAATTAQGGKTAGAPLPGLGTSYGHRTSGYTSHPATSPRA 211
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 212 GSALPDPQ--TASALPDPRAQA-----LPALAVISFLGLGLVAC 252
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

```
DB 212 GSSRPMDSTSAEDTSPALSSGSSKPRVSIPIWVRIAPVLLSLLSAGLIAFC 268

RESULT 72
US-09-989-723-517
/ Sequence 517; Application US/09989723
/ Patent No. US20020072092A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Ealon, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gottlieb, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C52
/ CURRENT FILING DATE: US/09/989,723
/ PRIOR APPLICATION NUMBER: 2001-11-19
/ PRIOR FILING DATE: 1997-06-16
/ PRIOR APPLICATION NUMBER: 60/049787
/ PRIOR FILING DATE: 1997-06-16
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/065186
/ PRIOR FILING DATE: 1997-11-12
/ PRIOR APPLICATION NUMBER: 60/065311
/ PRIOR FILING DATE: 1997-11-13
/ PRIOR APPLICATION NUMBER: 60/066770
/ PRIOR FILING DATE: 1997-11-24
/ PRIOR APPLICATION NUMBER: 60/075945
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/ PRIOR FILING DATE: 1998-06-04
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RESULT 73  
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Sequence 517, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Tyman, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C56  
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CURRENT FILING DATE: 2001-11-19  
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70	PRIOR FILING DATE: 1998-07-07	
71	PRIOR APPLICATION NUMBER: 60/091982	
72	PRIOR FILING DATE: 1998-07-07	
73	PRIOR APPLICATION NUMBER: 60/092182	
74	PRIOR FILING DATE: 1998-07-09	

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Guney, Austin L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C65
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13 PRIOR FILING DATE: 1998-07-09

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Query Match 9.5%; Score 125; DB 9; Length 332;  
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match 9.5%; Score 125; DB 9; Length 332;

Best Local Similarity 22.9%; Pred. No. 0.092; Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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Db 2 RLVLVLMGCLLPGEYALEGPEBISGFGDVTSLQCTYREELDRHKYCKRGKILFSRC 61
Qy 65 QGSPFLT--KGPSKLDNRA---DSRRSLWDGNFPLIINKLKIEDSYICEVEDQKEVQ 119
Db 62 SGTIYAEEGGETMGRVSIRDSRQEL-----SLIVTLNVLTLQDAGEVWCGEKKGPPES 117
Qy 120 LIVFGLTNSDTHLIQSGSLTTLTLESPPGSSBSVQCSRPKGNKIQGKTLVSQLE---- 175
Db 118 LLI-----SLFVPPGPC-----CPSPSPFTQ-----PLATTRLQPRAX 151
Qy 176 -----LQSSGWTCTVNLQNKVEPKIDIVPRASL-----PA--PPT 211
Db 152 AQQTQPPGLTSPGLYPAATTKQCKTGGAAPPLPETSQYGHERTSQYTGTSBHPATSPPA 211
Qy 212 GSALPDPQ--TASALDPDPAASA-----DPAALAVISFLGLGVAC 252
Db 212 GSRPPMQLDRTSADRTSPALSSGSSKRPVSLPMWRIIAPVLVLSLSAAGLIATFC 268

RESULT 78
US-09-990-442-517
; Sequence 517, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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2	PRIOR FILING DATE: 1998-06-05
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41	PRIOR FILING DATE: 1998-07-02
42	PRIOR APPLICATION NUMBER: 60/091633
43	PRIOR FILING DATE: 1998-07-02
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48	PRIOR APPLICATION NUMBER: 60/092182
49	PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 9; Length 332;  
Best Local Similarity 22.9%; Pred. No. 0.092;  
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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QY	65	QGSFLT--KGPSKLNDRA---DSRRSLMDQGNFLIIKLNKIEDSDTYICEVEDOKEVQ	119
Db	62	SGTLYAEBSGQETMKGRVSRDSRQEL---SLIVTLNLTLDQAGEYWCVEKRRGPDES	117
QY	120	LLVGLTNANSTHLLQGSLTLLTESPPGSSPSVQCSRPRKINIQGKTLVSQLE----	175
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QY	176	-----LQDSGWTCTVLONOKKVEKIDIVERASAL-----PA--PPT	211
Db	152	AQQTQPRPLTSPGLYPRATTAKQKGTAEARPLTQTSYGHEKRTSQYGTSPNRYATSPRA	211
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RESULT 80  
US-09-993-604-517  
Sequence 517, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Geritsen, Mary E.  
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APPLICANT: Godowski, Paul J.  
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APPLICANT: Gurney, Auerlin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C25  
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PRIOR APPLICATION NUMBER: 60/091978  
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 9; Length 332;  
Best Local Similarity 22.9%; Pred. No. 0.092;  
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RHLLVLQALPLA--ATGKNVVLGKGDVETLCTASQK-KSIQPHMKNSNOIKILGN 64  
DB 2 RLVLVLMGLLLPGVLEALGPEEISGFEDTVSLQCTTNEELDRKRWCKRGKGLFSRC 61  
QY 65 OGSFLL--KGPSKLDRA---DSRSLMDQGNFPLIKNLKIEDSDYVICEVEDQKEVQ 119  
DB 62 SCTVIAEEGQETMKGRVSIKRSQEL---SLVITLWMLTQDAGEWCGVEKKGPPBS 117  
QY 120 LLVGLGTANSDTHLLOGSGLTLLSPSSSSSVQCRSPKKNIGGKTLVSQLE---- 175

DB 118 LLI-----SLFVPGPC-----CPSPSPFTQ-----PLATRLQPRAK 151  
QY 176 -----LQSGWTCTVLOQKVEFKIDIVPASAL-----PA--PPT 211  
DB 152 AQQTQPPGLTSPGLYPAATKAGKTGAEPPLPCTQYGHERTSQYTGTSPHRATSPRA 211  
QY 212 GSALPDPQ--TASALPDPAPASA-----LPAALAVISPLLGIGLVAC 252  
DB 212 GSRPMPQLDSTSAEDTSPALSSGSKPRVSIPIWRIAPLVLTSLISAAGLIAFC 268

RESULT 81  
US-09-990-456-517  
Sequence 517, Application US/09990456  
Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deans, Luc  
APPLICANT: Batson, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC22  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: US/09/990,456  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 9; Length 332;  
Best Local Similarity 22.9%; Pred. No. 0.092;  
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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Qy 65 QGSFPL--KGPSKANDRA---DSRSIMDQGNFPLIKLKIEDSDTYICEVEDQKEVQ 119  
Db 62 SGTIAEEGGQETMKGRYSIRDSQEL---SLIVLWMLTLQDAGEWCGCEKGPDES 117  
Qy 120 LLVFLGLTANSDTHLLQGSGLTLTLSPGSSPSVOCSPRGKNIQGGKTLVSOLE---- 175  
Db 118 LLI-----SLVFPFGPC-----CPSPSPFQ-----PLATTRLQPKAK 151  
Qy 176 -----LQDSGWTCTVLQNKVKEFKIDIVPASAL-----PA--PPT 211  
Db 152 AQOTQPGCLTSPGLYPAATTAKGKTGAAPLPFGNSYGHERTSQYTGTSHPATSPPA 211  
Qy 212 GSALDPPQ--TASALDPPPAASA-----LPAALAVISFLGLGLVAC 252  
Db 212 GSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRIIAPVLVLLSLSAAGLIAFC 268

## RESULT 82

US-09-989-721-517  
Sequence 517, Application US/09989721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Aekhenazi, Avi J.  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Auecin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC55  
CURRENT APPLICATION NUMBER: US/09/989,721  
CURRENT FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1997-06-16  
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[illegible]

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Oy       65 QGSFLT---KGPSKUNDA---DSRRSLWDGNPFLIIKNLKIEDSDPYICEVEDOKKEVPQ   119
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Db        62 SGTIVAEEGGETMKGRVSIRDSROEL---SLVTIWNLTLDAGETWCGVEKRGPDES   117
Oy       120 LLVLGELTRANSPTHLLQGOSLTLTLTESPPGSSPVQCSPRGKNIQGGKTLSVSOLE----   175
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Db       118 LLT-----SLFFFPBGCS-----CPSPSEPTIQ-----PLATTRLQPRAK   151
Oy       176 -----LQDSCWTCTVTLONQKVFEKIDIVPRASAL-----PA--PPT   211
Db       152 AQQTPPEPLTSPPGIYPATTAQCKTGKAEPPLGTSGYGHERTSQYTGSTPHPATSPBA   211
Oy       212 GSALLPDPO--IASALPPRPASA-----LPAIAVISFLIGLGIGAC   252
Db       212 GSSRPQMQLDSTSAEDTSPALSSSKRPVSI PMVRILA PVLILTSLISAAGLIAFC   268

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US-09-978-295A-216
Sequence 216, Application US/0978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
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APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P26301C11
CURRENT APPLICATION NUMBER: US/09/978, 295A
CURRENT FILING DATE: 2001-10-15
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62	PRIOR APPLICATION NUMBER: 60/081071	62	PRIOR FILING DATE: 1998-05-07
63	PRIOR FILING DATE: 1998-04-08	63	PRIOR APPLICATION NUMBER: 60/084643
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65	PRIOR FILING DATE: 1998-04-08	65	PRIOR APPLICATION NUMBER: 60/085339
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Query Match 9.5%; Score 125; DB 9; Length 332;  
Beet Local Similarity 22.9%; Pred. No. 0.092;  
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13

QY 8 RHLVLVQLALLDPA--ATGKNKVLGCKKDDYTELCTASOK-KSIOFMKKSNOIKITGN 64  
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 QY 65 QSSFLT--KGPSKLNDRA--DSRSLMDQGNPLIIKXLIKESDYICEVEDOKEVQ 119  
 Db 62 SGTYVAEEEOQETMKRVSIRDSROEL---SLIYTNLNLTLDOAGEWCKVEGRGPD 117  
 QY 120 LTVFGLTANSDTHLLQGSULTLTLSRPPSSPSVQCRRPKNKIQGKTKLSVQLE--- 175  
 Db 118 LLI-----SLTFVFPGPC-----CPSPSPFTQ-----PLATTPLOPKAK 151  
 QY 176 -----LDQSGTWTCTVLQONKVEFKIDIVPRASAL-----PA--PPT 211  
 Db 152 AQQTPRGSLSPELVPAATTAKQKTKGALARPPLGTSQYGHERTSQYGTSPHATSRA 211  
 QY 212 GSAALPDDQ--TASALDPPRAAS-----LPALATVTSFLIGLGLVAC 252  
 Db 212 GSSRPFWQDSTSAEDTSPALSSGSGSKRPVSIPIWRIILAPVLVLISLSAAGLIAFC 268

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1 RESULT 84
2 US-09-992-598--517
3 Sequence 517, Application US/09992598
4 Patent No. US20020160384A1
5 GENERAL INFORMATION:
6 APPLICANT: Ashkenazi, Avi J.
7 APPLICANT: Baker, Kevin P.
8 APPLICANT: Bortstein, David
9 APPLICANT: Desnoyers, Luc
10 APPLICANT: Eaton, Dan L.
11 APPLICANT: Ferrara, Napoleone
12 APPLICANT: Fong, Sherman
13 APPLICANT: Garber, Hanspeter
14 APPLICANT: Gerritsen, Mary E.
15 APPLICANT: Goddard, Audrey
16 APPLICANT: Godowski, Paul J.
17 APPLICANT: Grimaldi, J. Christopher
18 APPLICANT: Gurney, Austin L.
19 APPLICANT: Kijavini, Ivar J.
20 APPLICANT: Napier, Mary A.
21 APPLICANT: Pan, James
22 APPLICANT: Paoni, Nicholas F.
23 APPLICANT: Roy, Margaret Ann
24 APPLICANT: Stewart, Timothy A.
25 APPLICANT: Tumas, Daniel
26 APPLICANT: Watanabe, Colin K.
27 APPLICANT: Williams, P. Mickey
28 APPLICANT: Wood, William I.
29 APPLICANT: Zhang, Zemin
30 TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
31 TITLE OF INVENTION: Acids Encoding the Same
32 FILE REFERENCE: P2730P1C20
33 CURRENT APPLICATION NUMBER: US/09/992,598
34 CURRENT FILING DATE: 2001-11-14
35 PRIOR APPLICATION NUMBER: 60/049787

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; PRIOR FILING DATE: 1998-07-09

Query Match      9.5%; Score 125; DB 9; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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RESULT 85
US-09-978-697-216
; Sequence 216, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Efron, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.

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APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
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; PRIOR FILING DATE: 1998-07-09
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QY      176 -----LQDSGWTCTVLNQNKKVEFKDIVPRASAL-----PA--PPT 211
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RESULT 87
US-09-978-192A-216
; Sequence 216, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
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APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
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APPLICANT: Kuo, Sophia S.  
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APPLICANT: Stewart, Timothy A.  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
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Query Match 9.5%; Score 125; DB 9; Length 332;

Best Local Similarity 22.9%; Fred. No. 0.092; Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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QY 8 RHLLVLQALALPA--ATQGNKVVLGKGGDTVELTCTASOK-KSIQFHKNSNQIKILGN 64
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| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 RLVLVLMGCLLPGLYALLEGPEETISFEGDTVSLOCTYBELRDKRKYCRKGILFSC 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 65 QGSFLT-KPSTLNDRA---DSRRSLMDQGNPFLIKLIKIEDSDTYICEVEDOKEEVO 119
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 SGTIVAEEGQETMKGRVSIKRSRQL---SLIVLWLVLTQDAEYWGCVGKRGPDSS 117
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 120 LVFGLTANSDTLLLOGQSLTLTLESPGSSPSVQCRSRGKNIOGKTLISOLE---- 175
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 118 LLI-----SLVFPGPC-----CPSPSPPTQ-----PLATTRLQPKAK 151
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 176 -----LDSGTWTCVTLQNKVEFKIDIVRASAL-----PA--PPT 211
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 152 AOOTPGPLTSPGLYPAATTAKGKGALNPLPGTSQYGHERTSYTGTSHPAISPAA 211
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 212 GSALPDPO--TASALPDPPAASA-----LPAAIAVISFLLGLGLGVAC 252
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 212 GSSRPQMQLDSTSAEDTSPALSSGSKPRVSIPIWVILAPVLVLLSLAAGLIAPC 268
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 88
US-09-999-832A-216
/ Sequence 216, Application US/09999832A
/ Publication No. US20020192706A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerder, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James;
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C63
/ CURRENT APPLICATION NUMBER: US/09/999,832A
/ CURRENT FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
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/ PRIOR APPLICATION NUMBER: 60/065311
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16	PRIOR FILING DATE: 1998-04-30
17	PRIOR APPLICATION NUMBER: 60/084366
18	PRIOR FILING DATE: 1998-05-05
19	PRIOR APPLICATION NUMBER: 60/084414
20	PRIOR FILING DATE: 1998-05-06
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23	PRIOR APPLICATION NUMBER: 60/084637
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49	PRIOR APPLICATION NUMBER: 60/085704
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51	PRIOR APPLICATION NUMBER: 60/085697

Query Match	9.5%	Score 125;	DB 9;	length 332;
Best Local Similarity	22.9%;	Pred. No. 0.092;		
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				Indels 82;
				Gaps 13;

[illegible]

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Db 152 AAOGTOPGLTSPGLVYAATTAKQSKTGAEAPPLPGTSQYGHERTSQTTSPPHATSPPA 211  
QY 212 GSALPDPO--TASALDPDPPAASA-----LPALAVISFLLGLGLGVAC 252  
Db 212 GSSRPQMJDSTSAEDTSPALSSGSSKPRVSIPIWVILAPVLVLTLSAAGLIANC 268  
RESULT 89  
US-09-989-735-517  
Sequence 517, Application US/09989735  
Publication No. US20020193299A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C61  
CURRENT FILING DATE: 2001-11-19  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-19

1	PRIOR APPLICATION NUMBER: 60/089952
2	PRIOR FILING DATE: 1998-06-19
3	PRIOR APPLICATION NUMBER: 60/090246
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8	PRIOR FILING DATE: 1998-06-22
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10	PRIOR FILING DATE: 1998-06-23
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16	PRIOR FILING DATE: 1998-06-24
17	PRIOR APPLICATION NUMBER: 60/090435
18	PRIOR FILING DATE: 1998-06-24
19	PRIOR APPLICATION NUMBER: 60/090444
20	PRIOR FILING DATE: 1998-06-24
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22	PRIOR FILING DATE: 1998-06-24
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35	PRIOR APPLICATION NUMBER: 60/090678
36	PRIOR FILING DATE: 1998-06-25
37	PRIOR APPLICATION NUMBER: 60/090650
38	PRIOR FILING DATE: 1998-06-25
39	PRIOR APPLICATION NUMBER: 60/090634
40	PRIOR FILING DATE: 1998-06-25
41	PRIOR APPLICATION NUMBER: 60/090635
42	PRIOR FILING DATE: 1998-06-25
43	PRIOR APPLICATION NUMBER: 60/090656
44	PRIOR FILING DATE: 1998-06-25
45	PRIOR APPLICATION NUMBER: 60/090862
46	PRIOR FILING DATE: 1998-06-26
47	PRIOR APPLICATION NUMBER: 60/090863
48	PRIOR FILING DATE: 1998-06-26
49	PRIOR APPLICATION NUMBER: 60/091360
50	PRIOR FILING DATE: 1998-07-01
51	PRIOR APPLICATION NUMBER: 60/091478
52	PRIOR FILING DATE: 1998-07-02
53	PRIOR APPLICATION NUMBER: 60/091544
54	PRIOR FILING DATE: 1998-07-01
55	PRIOR APPLICATION NUMBER: 60/091519
56	PRIOR FILING DATE: 1998-07-02
57	PRIOR APPLICATION NUMBER: 60/091626
58	PRIOR FILING DATE: 1998-07-02
59	PRIOR APPLICATION NUMBER: 60/091633
60	PRIOR FILING DATE: 1998-07-02
61	PRIOR APPLICATION NUMBER: 60/091787
62	PRIOR FILING DATE: 1998-07-07
63	PRIOR APPLICATION NUMBER: 60/091982
64	PRIOR FILING DATE: 1998-07-07
65	PRIOR APPLICATION NUMBER: 60/092182
66	PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 9; Length 332;  
 Best Local Similarity 22.9%; Pred.No. 0.092;  
 Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13

QY 8 RHLLVLDLALPP--ATGGNKVVVLGGKGDPTVELCTASQK-KSLOFHKKNSNOQIKLGN 64  
 |::: ||| |::: |::: |||| |::: |::: |

Db 2 RLIVLLMGCLLLPGVEALEGPBEIISGFGDTIVSLQCTYREELTRDHRKRYCKRGKGIILPSPRC 61

Oy 65 QGSFLL--KGP&KANDRA---DSRSLMDQGNFPIILKNLKI&SDPTIYICEV&QKEVQ 119

Db 62 SGTIYAE&G&Q&ETMK&R&SIR&DSR&EL---SLIVTLVNLTLQ&AGEW&GV&ER&GPDES 117

Oy 120 LTVF&GLT&NSDTHLLQ&GS&LTLTLES&PGSS&SVQ&SR&GN&IQ&G&TL&SV&OLE--- 175

Db 118 LLL-----SLFVFP&PC-----CP&SP&PT&Q-----PL&TRT&LP&K&K 151

Oy 176 -----LQDS&TW&TCV&LQ&N&Q&K&VE&K&ID&IV&P&AS&L-----P&A---P&PT 211

Db 152 A&O&T&P&G&L&T&S&P&G&L&P&A&T&T&A&K&G&T&G&A&E&A&L&P&T&S&O&Y&G&H&R&T&S&O&Y&T&G&T&S&P&H&A&T&S&P&A 211

Oy 212 GS&L&P&P&O---T&AS&L&D&P&P&AS&-----L&P&L&A&V&IS&F&L&G&L&G&L&V&A&C 252

Db 212 G&S&R&P&P&M&Q&L&D&T&S&A&E&T&S&P&A&L&S&G&S&K&R&V&S&I&P&M&R&I&A&P&V&L&I&S&L&S&A&A&G&L&A&F&C 268

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1  RESULT 90
2  US-09-990-444-517
3  ; Sequence 517, Application US/09990444
4  ; Publication No. US2002019300A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Ashkenazi, Avi J.
7  ; APPLICANT: Baker, Kevin P.
8  ; APPLICANT: Botstein, David
9  ; APPLICANT: Desnoyers, Luc
10 ; APPLICANT: Eaton, Dan L.
11 ; APPLICANT: Ferrara, Napoleone
12 ; APPLICANT: Fong, Sherman
13 ; APPLICANT: Gerber, Hanspeter
14 ; APPLICANT: Gerritsen, Mary E.
15 ; APPLICANT: Goddard, Audrey
16 ; APPLICANT: Godowski, Paul J.
17 ; APPLICANT: Grimaldi, J. Christopher
18 ; APPLICANT: Gurney, Austin L.
19 ; APPLICANT: Kijavits, Ivar J.
20 ; APPLICANT: Napier, Mary A.
21 ; APPLICANT: Pan, James
22 ; APPLICANT: Paoni, Nicholas F.
23 ; APPLICANT: Roy, Margaret Ann
24 ; APPLICANT: Stewart, Timothy A.
25 ; APPLICANT: Tuma, Daniel
26 ; APPLICANT: Watanabe, Colin K.
27 ; APPLICANT: Williams, P. Mickey
28 ; APPLICANT: Wood, William I.
29 ; APPLICANT: Zhang, Zemin
30 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
31 ; FILE REFERENCE: P2730P1C19
32 ; CURRENT APPLICATION NUMBER: US/09/990,444
33 ; PRIOR FILING DATE: 2001-11-14
34 ; PRIOR APPLICATION NUMBER: 60/049787
35 ; PRIOR FILING DATE: 1997-06-16
36 ; PRIOR APPLICATION NUMBER: 60/062250
37 ; PRIOR FILING DATE: 1997-10-17
38 ; PRIOR APPLICATION NUMBER: 60/065186
39 ; PRIOR FILING DATE: 1997-11-12
40 ; PRIOR APPLICATION NUMBER: 60/065311
41 ; PRIOR FILING DATE: 1997-11-13
42 ; PRIOR APPLICATION NUMBER: 60/066770
43 ; PRIOR FILING DATE: 1997-11-24
44 ; PRIOR APPLICATION NUMBER: 60/075945
45 ; PRIOR FILING DATE: 1998-02-25
46 ; PRIOR APPLICATION NUMBER: 60/078910
47 ; PRIOR FILING DATE: 1998-03-20
48 ; PRIOR APPLICATION NUMBER: 60/083322
49 ; PRIOR FILING DATE: 1998-04-28
50 ; PRIOR APPLICATION NUMBER: 60/084600
51 ; PRIOR FILING DATE: 1998-05-07
52 ; PRIOR APPLICATION NUMBER: 60/087106
53 ; PRIOR FILING DATE: 1998-05-28

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[illegible][illegible]

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      9.5%; Score 125; DB 9; Length 332;
Beat Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13

OY      RHLVLVQLALLPA--ATQGNKVYLGGKDDTYELTCTASQK-KSIQFHHKNSNOIKLGN 64
DB      2 RLVLVLWGCLLLPGVEALEGPEEISGFEDDTVSLOCTYNEELDRHKVCCKRGKGLFSRC 61
OY      QGSFLT--KGPEKLNDRA---DSRSLMQGNFPILIKLKIEDSDTYICEVEDQKEEVQ 119
DB      62 SGTIAEEGGQTMTMGGRVISIRSRQEL-----SLVTLMNLTLDAGEYTCGYEKKGPDSS 117
OY      120 LVLFGSLTNSDTHLLQGQSRLTLTESPPGSSPVOCRSFRGNIGSGKTLSYSOLE---- 175
DB      118 LLI-----SLVFVPGPC-----CPSPSPSTPFG-----PLATTRIQPKAX 151

OY      176 -----LDQSGTTCTCYLVNQKKVVERKIDIVPPASAL-----PA--PT 211
DB      152 AQQTGPGLTSPGLTPAATTAKQKGAEPPLPGNSGYGHERTSQYTGSTPHAPTSPA 211
OY      212 GSALDPDPC--TKSALVDPPASA-----LPALAVISFLILGLGLVAC 252
DB      212 GSSRPQMUDSTSADDTSPALSSGSSSKPRVISIPMWRTILAPVLVLSSLASAGLIAFC 268

RESULT 91
US-09-991-181-517
; Sequence 517, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Geber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC53
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945

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3	PRIOR FILING DATE: 1998-03-20
4	PRIOR APPLICATION NUMBER: 60/0833222
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6	PRIOR APPLICATION NUMBER: 60/0846000
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8	PRIOR APPLICATION NUMBER: 60/0871066
9	PRIOR FILING DATE: 1998-05-28
10	PRIOR APPLICATION NUMBER: 60/0876077
11	PRIOR FILING DATE: 1998-06-02
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61	PRIOR FILING DATE: 1998-06-11
62	PRIOR APPLICATION NUMBER: 60/0891050
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67	PRIOR FILING DATE: 1998-06-16
68	PRIOR APPLICATION NUMBER: 60/0895144
69	PRIOR FILING DATE: 1998-06-16
70	PRIOR APPLICATION NUMBER: 60/0895322
71	PRIOR FILING DATE: 1998-06-17
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73	PRIOR FILING DATE: 1998-06-17

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PRIOR APPLICATION NUMBER:	60/091544
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PRIOR APPLICATION NUMBER:	60/091519

1 PRIOR FILING DATE: 1998-07-02  
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4 PRIOR APPLICATION NUMBER: 60/091633  
5 PRIOR FILING DATE: 1998-07-02  
6 PRIOR APPLICATION NUMBER: 60/091978  
7 PRIOR FILING DATE: 1998-07-02  
8 PRIOR APPLICATION NUMBER: 60/091982  
9 PRIOR FILING DATE: 1998-07-02  
10 PRIOR APPLICATION NUMBER: 60/092182  
11 PRIOR FILING DATE: 1998-07-03

Query Match	9.5%;	Score 125;	DB 9;	Length 332;
Best Local Similarity	22.9%;	Pred. No. 0.092;		
Matches 68;	Conservative 38;	Mismatches 109;	Indels 82;	Gaps 13;

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QY      RHLLVLTQATALLPA---ATGNGKVVVLGKKGGDPVLTCTASOK--KSIQFMKNSNDIKILGN 64
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      2 RLIVVLMGCLLPGIEALGEPPEIIGFEDIVLSLOCTYRELRLRHKKYMKCRKGILLRSRC 61
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      65 QGSFLT--KGPSKLANDRA---DSRSLMDQGNFPLIINKLIKEDSDTYICEVEDQKEVQ 119
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      62 SGTIVAEESQGETMKGRVSRISDRSQEL-----SLVITLNNLLTDAGEWCCVEKRGPD 117
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      120 LLVFGLTASDPHLLQGSGLTITLESPPGSSPSVCCRPKKNIQGKCTLVSQLE---- 175
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      118 LLI-----SLFVPPGPC-----CPSPSPSTFQ-----PLATTRLQPKAK 151
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      176 -----LDQSGTWTCTVLQNOKEVERKIDIVPRA$AL-----PA--PPT 211
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      152 AAGTQPPGLTSPCLVPAATTAQKGTGA$APLPLPQTSQYGHERTSQYGTGSPHPAT$PPA 211
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      212 G$ALPDPQ--TASALPDP$P$A$A-----LP$ALANTISPLUGLGLVAC 252
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      212 G$SRP$PQD$T$AEDT$P$AL$SSG$K$P$V$T$P$W$RI$A$P$V$V$T$LS$A$A$G$LA$F$C 268
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

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RESULT 92  
US-09-985

; Sequence 517, Application US/09989730  
; Publication No. US20020197674A1

1 APPLICANT: Ashkenazi, Avi J.  
 2 APPLICANT: Baker, Kevin P.  
 3 APPLICANT: Botstein, David  
 4 APPLICANT: Desnovers, Luc  
 5 APPLICANT: Eaton, Dan L.  
 6 APPLICANT: Ferrara, Napoleone  
 7 APPLICANT: Fong, Sherman  
 8 APPLICANT: Gerber, Hanspeter  
 9 APPLICANT: Gerritsen, Mary E.  
 10 APPLICANT: Goddard, Audrey  
 11 APPLICANT: Godowski, Paul J.  
 12 APPLICANT: Grimaldi, J. Christopher  
 13 APPLICANT: Gurney, Austin L.  
 14 APPLICANT: Kijavini, Ivar J.  
 15 APPLICANT: Napier, Mary A.  
 16 APPLICANT: Pan, James  
 17 APPLICANT: Paoni, Nicholas P.  
 18 APPLICANT: Roy, Margaret Ann  
 19 APPLICANT: Stewart, Timothy A.  
 20 APPLICANT: Tumas, Daniel  
 21 APPLICANT: Watanabe, Colin K.  
 22 APPLICANT: Williams, P. Mickey  
 23 APPLICANT: Wood, William I.  
 24 APPLICANT: Zhang, Zemin  
 25 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 26 FILE REFERENCE: P2730P1C69  
 27 CURRENT APPLICATION NUMBER: US/09/989,730  
 28 CURRENT FILING DATE: 2001-11-20  
 29 PRIOR APPLICATION NUMBER: 60/049787  
 30 PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/068225-0	
PRIOR FILING DATE: 1997-10-17	
PRIOR APPLICATION NUMBER: 60/065186	
PRIOR FILING DATE: 1997-11-12	
PRIOR APPLICATION NUMBER: 60/065311	
PRIOR FILING DATE: 1997-11-13	
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PRIOR FILING DATE: 1997-11-24	
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PRIOR APPLICATION NUMBER: 60/078910	
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PRIOR APPLICATION NUMBER: 60/083322	
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PRIOR FILING DATE: 1998-06-12	
PRIOR APPLICATION NUMBER: 60/089440	

[illegible][illegible]

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; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

```

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Query Match          9.5%; Score 125, DB 9, Length 332,
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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QY      8 RHLLVLQALALPA--ATQGNKVVLGKGDVTELTCTASOK-KSIQFMKNSNQIKILGN 64
      2 RLVLVLMGCLLRLGYALSGEPERISGEGDTVSLQCTYABEILDRHKYCRKGILFSRC 61
QY      65 QGSFLLT-KGPSKLANDRA--DSRRSLMDQGNFPLIKKLIKIEDSDTYICEVEDQKEEQY 119
      62 SGTYAEEGSGEETMKRVSIRDSRQL-----SLIVLMLVTLQDAEYVCGYEKRQPDSS 117
QY      120 LLVFGLTANSDFHLLOGQSILTLTLESPGSSPEVQCRSPRGKNIQCGKTLVSQLE---- 175
      118 LLI-----SLVFPGPC-----CPPSPSPFQ-----PLATTRLQPKAK 151
QY      176 -----LQDSGTWTCVTLQNKQKVEFKDIVPRASAL-----PA--PPT 211
      152 AQGTQPGTLSPGLYPAATTAQKQKGAEPPLGTSQYGHERTSOYTSPPHATSPPA 211
QY      212 GSALPDPQ--TASALPDPAPASA-----LPAALAVISFLGLGIVAC 252
      212 GSRPFWQDSTSAEPTSPALSSGSKPRVSTPMRIAPVLVLSLSAAGLIAC 268
Db

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RESULT 93
US-09-990-436-517
; Sequence 517, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC14
; CURRENT APPLICATION NUMBER: US/09/990,436
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-10

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6	PRIOR FILING DATE: 1998-06-11
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9	PRIOR APPLICATION NUMBER: 60/089440
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15	PRIOR APPLICATION NUMBER: 60/089532
16	PRIOR FILING DATE: 1998-06-17
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18	PRIOR FILING DATE: 1998-06-17
19	PRIOR APPLICATION NUMBER: 60/089598
20	PRIOR FILING DATE: 1998-06-17
21	PRIOR APPLICATION NUMBER: 60/089599
22	PRIOR FILING DATE: 1998-06-17
23	PRIOR APPLICATION NUMBER: 60/089600
24	PRIOR FILING DATE: 1998-06-17
25	PRIOR APPLICATION NUMBER: 60/089653
26	PRIOR FILING DATE: 1998-06-17
27	PRIOR APPLICATION NUMBER: 60/089801
28	PRIOR FILING DATE: 1998-06-18
29	PRIOR APPLICATION NUMBER: 60/089907
30	PRIOR FILING DATE: 1998-06-18
31	PRIOR APPLICATION NUMBER: 60/089908
32	PRIOR FILING DATE: 1998-06-18
33	PRIOR APPLICATION NUMBER: 60/089947
34	PRIOR FILING DATE: 1998-06-19
35	PRIOR APPLICATION NUMBER: 60/089948
36	PRIOR FILING DATE: 1998-06-19
37	PRIOR APPLICATION NUMBER: 60/089952
38	PRIOR FILING DATE: 1998-06-19
39	PRIOR APPLICATION NUMBER: 60/090246
40	PRIOR FILING DATE: 1998-06-22
41	PRIOR APPLICATION NUMBER: 60/090252
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43	PRIOR APPLICATION NUMBER: 60/090254
44	PRIOR FILING DATE: 1998-06-22
45	PRIOR APPLICATION NUMBER: 60/090349
46	PRIOR FILING DATE: 1998-06-23
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48	PRIOR FILING DATE: 1998-06-23
49	PRIOR APPLICATION NUMBER: 60/090429
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70	PRIOR FILING DATE: 1998-06-25
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72	PRIOR FILING DATE: 1998-06-25
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11	PRIOR FILING DATE: 1998-06-26
12	PRIOR APPLICATION NUMBER: 60/091360
13	PRIOR FILING DATE: 1998-07-01
14	PRIOR APPLICATION NUMBER: 60/091478
15	PRIOR FILING DATE: 1998-07-02
16	PRIOR APPLICATION NUMBER: 60/091544
17	PRIOR FILING DATE: 1998-07-01
18	PRIOR APPLICATION NUMBER: 60/091519
19	PRIOR FILING DATE: 1998-07-02
20	PRIOR APPLICATION NUMBER: 60/091626
21	PRIOR FILING DATE: 1998-07-02
22	PRIOR APPLICATION NUMBER: 60/091633
23	PRIOR FILING DATE: 1998-07-02
24	PRIOR APPLICATION NUMBER: 60/091978
25	PRIOR FILING DATE: 1998-07-07
26	PRIOR APPLICATION NUMBER: 60/091982
27	PRIOR FILING DATE: 1998-07-07
28	PRIOR APPLICATION NUMBER: 60/092182
29	PRIOR FILING DATE: 1998-07-09

Query Match	9.5%;	Score 125;	DB 9;	Length 332;
Best Local Similarity	22.9%;	Pred. No. 0.092;		
Matches 68;	Conservative 38;	Mismatches 109;	Indels 82;	Gaps 13;

```

Qy      8 RHLLVLLOALLPA---ATGKNVVLGGKGDVYELTCTASOK-KSIOFMKNSNQIKILGN 64
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      2 RLIVLLMGCLLLPGYALEGPEEIGFEGDVTYSLOCTYRELRDRHKRYCKCKGAILSRSC 61
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      65 QGSEFLT-KGFSKLNDRA---DSRSLWDQGFPLIINKLIEDSDTYICEVEDOKEVQ 119
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      62 SGTIVAEEGEOMETKGRVSIKDSRQEL---SLIYTLNLLTLODAGEWCKVEGRGPDSS 117
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      120 LTVFGLTANSDTHLLQGQSLTLTSPGGSSPVQCRPRKKNIQGQKTLVSQLE---- 175
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      118 LLI-----SLTFVPPGC-----CPSPSPFTFO-----PLATTLLOPKAK 151
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      176 -----LQDSGTWTCVLOKQKVEERKIDIVPRASAL-----PA---PPT 211
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      152 AAGTQPPGLTSPGLVPAATTAKQGTGAEDAPLPCTSQYGHERTSQYGTGSPHATSPPA 211
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      212 GSAIPLPPQ--TASALDPPASA-----LPALANVISFVLGIGLQVAC 252
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      212 GSSRPWQIDSTSAEDTSPALSSGSKKERVASIPWRIIAPVLVLLSLASGALPAC 268
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RESULT 94  
US-09-993-687-517  
Sequence 517, Application US/09993687  
Publication No. US20020198149A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Boesteven, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Andrew  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.

APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C11  
CURRENT APPLICATION NUMBER: US/09/393,687  
CURRENT FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066770  
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PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
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31	PRIOR APPLICATION NUMBER: 60/091633
32	PRIOR FILING DATE: 1998-07-02
33	PRIOR APPLICATION NUMBER: 60/091978
34	PRIOR FILING DATE: 1998-07-07
35	PRIOR APPLICATION NUMBER: 60/091982
36	PRIOR FILING DATE: 1998-07-07
37	PRIOR APPLICATION NUMBER: 60/092182
38	PRIOR FILING DATE: 1998-07-09



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PRIOR APPLICATION NUMBER:	60/091978
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/091982
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/092182
PRIOR FILING DATE:	1998-07-09

Query Match 9.5%; Score 125; DB 10; Length 332;

Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

8 RHLLVLQALLPA--ATQGNKVLGKKDVELTCTASQK-KSIQFHWKNSNQIKILGN 64

Db 2 RLVLWGCLLPGEALGPEISGFEGDVSLOCTYREELRDHRKYWCCKGGLFSRC 61

65 QGSFLT--KGPSKLDRA---DSRSLWDOGNFPLIKNLKIEDSDTYICEVEDOKEVEQ 119

62 SGTIYAEFGOETMKGPVSI PDSBOI-----SITVTIWNITLODAGEYWCGEVKEKGPDES 117

[illegible][illegible]

DB 118 LLI-----SLFVFPQC-----CPPSPPTFG-----PLATIRLQPKAK 151

176 -----LQDSGTWCTVLQÑQKVEFKIDIVPRASAL-----PA--ppt 211

Db 152 AQQTOPGLTSPGLYPATTAKQKGTGAEPPLPQTSQYGHERTSQYTGTSPPHATSPRA 211

212 GSALPDPQ--TASALPDPASA-----LPALAVISFLGLGVAC 252

Db 212 GSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRILAPVLVLLSLLSAAGLIAFC 268

RESULT 96  
US-09-978-189-216  
Sequence 216, Application US/09978189  
Publication No. US20030004102A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kliauin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      9.5%; Score 125; DB 10; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;
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QY      8 RHLLVLLQLALLPA--ATGQNKVVLGKKGDVTVELTJTASQK-KSIQFHKMKNISQIKILGN 64
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QY      65 QGSFLT--KGPSKLANDRA---DSRRSLMDQGNPLIINKUKIEDSDTYICEVEDQKEEYQ 119
DB      62 SGTIVAEEGQETMKRQVSRDROBL-----SLIVLMLVLTLDADAEYWCGEYKRPDDS 117
QY      120 LLVGLTANSDTHLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQGLE---- 175
DB      118 LLI-----SLVVFPGPC-----CPPSPPTFQ-----PLATRLQPKAK 151
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QY      176 -----LQDSGTCTFVLQNKYEFKIDIVPRASAL-----PA--PPT 211
DB      152 AQTQPGGLTSPGLYPAATTAQGKTGAAPPLPCTSYGCHRTSQYGTSPHATSPRA 211
QY      212 GSALPDPQ--TASALPDPAPASA-----LPALAVISFLIGLGVAC 252
DB      212 GSRPPMQLDSTYSADTSPALSSGSSKRPVSIPIWRIIAPVVLVLTSLASGLIAFC 268

RESULT 97
US-09-997-653-517
; Sequence 517, Application US/0997653
; Publication No. US20030008297A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Geider, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 10; Length 332;  
Best Local Similarity 22.9%; Pred. No. 0.092;  
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RHLLVLTALPPA-ATQGNKVVVLGKKGDTVELTCTASQK-KSIQFHWKSNQIKILGN 64  
DB 2 RLVLWGLCLLPGEVLEGPBEISGEGDVTSLQCTYREIRDRHKRYKCRKGGILFSRC 61

QY 65 OGSFLT-KGPSKLANDRA---DSRSGLMDQGNFPLIIKNUKIBSDTYICEVDEKEEYQ 119  
DB 62 SGTIVAEERGOETMKRVRISROEJL---SLIVLWNLTLDDAGEYWCGEKRPDSS 117  
QY 120 LVLVFGTANSDFHLOGOSLTLTLLESPPGSSPEVQGRSPRGKNIQGGKTLVSQLE--- 175  
DB 118 LVL-----SLVFPFGPC-----CPSPSPFFQ-----PLATRLQPKAK 151  
QY 176 -----LQDSCGTCTVLQONQKYEFKIDVPRASAL-----PA--PPT 211  
DB 152 AOGTQPPGLTSPFLYPAATTAKGKGAGAPLPFGTSQYGHERTSQYTGSPHATSPPA 211  
QY 212 GSALPPOC--TASALDPPASA-----LPAALAVISFLGLGLGVAC 252  
DB 212 GSRPFWQDSTSAEDTSPALSSGSKPRVSIPIWRIILAPVLVLSLSAAGLIAC 268

RESULT 98  
US-09-993-667-517  
Sequence 517, Application US/09993667  
Publication No. US2003002187A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deanoyere, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferreira, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
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APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C4  
CURRENT APPLICATION NUMBER: US/09/993,667  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-18

[illegible]

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Oy     65 QGSFLT--KGPSKINDRA---DSRRSLMDGFNPLIIKLKIEDSDTYICEVEDQKEEVQ 119
Dd     62 SGTIVAELEGEMTKGVSRIDSNQEL-----SLVTLMNLTDQAGEVWCVEVKRPSES 117
Oy     120 LTVFLGLTRANSDTHLLQGQSITLTLETSPPGSSPSVQCSSPRGKNIQCGKTLSVSQLE---- 175
Dd     118 LLI-----SLVFPPGPC-----CPPSPSPTQ-----PLATTRLOPKAX 151
Oy     176 -----LDQSGWTCTVLONQKVFEKIDIYRASAL-----PA--PPT 211
Dd     152 AAGTQPGLTSPGIYPATTAKOGKTGAEPPLFGTSQYGHERTSQYTGISPHPTSTPA 211
Oy     212 GSALPDPO--TASALPDPPASA-----LPALAVISFLLGLGLGVAAC 252
Dd     212 GSKRPQJDBSTDHEDISPALSQSSKPRVISIPMWRILAPVLVLISSLAAGLIAFC 268

RESULT 99
US-09-997-428-517
Sequence 517 Application US/09997428
Publication No. US20030027162A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyere, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kljavin, Iyar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC44
CURRENT APPLICATION NUMBER: US/09/997,428
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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Qy      65 QGSFLT--KGPSKLNDR---DSRSLMDQGNFPLIKKLTIEDSDTYICEVEDQKEEYQ 119
      62 SGTIVAEEGCGETMGCRVSIKRSQEL---SLIVTLMVLTQDAGEYWCYKRGKGPDES 117
Db      120 LIVFGLTANSDTHLIQGSLTTLTSSPPSSPSVQCRSPRGKNIQGGKTLVSQLE--- 175
      118 LLI-----SLFVFPGPC-----CPSPSPPTFQ-----PLATTRLQPYAK 151
Qy      176 -----LQDSGTCTCTVLQNKYKFKIDIVPPASAL-----PA--PPT 211
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Db      212 GSALPDPPQ--TASALPDPPASA-----LPALAVISFLGLGLGVAC 252
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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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 PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 10; Length 332;  
 Best Local Similarity 22.9%; Pred. No. 0.092;  
 Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RHLVLQALIPA--ATQGNKVVLGKKDFTVLTCTASOK-KSIOFHKNSNOIXILGN 64  
 DB 2 RLVLVLMGCLLPGEALGEBEISGFGDIVSLQCTREELRDHKKYCKRGKGLFGR 61  
 QY 65 QGSFLT--KGPSKLNDR---DSRSWLDQGNFPLINLKIEDSDTYICEVEDQKEVQ 119  
 DB 62 SGTIVAESEGQETMKGRVSRDSRQEL---SLIVLWNLTLQDAGEVWCGVEKKGPDS 117  
 QY 120 LTVFGLTANSDTHLQGSGLTTLTSPGSSPSVQCRPRGKNIGGKTLISVQLE---- 175  
 DB 118 LLI-----SLVFPFGPC-----CPSPSPFTQ-----PLATTRLQPRAX 151  
 QY 116 -----LQDSGTWTCTVLQONQKVEPKIDIVPASAL-----PA--PPT 211  
 DB 132 AQCTOPPGILTSPLGLYPAATTKAGKTGAAPLPETSGYGHERTSQYTGSTPHRTSPFA 211  
 QY 212 GSALPDPQ--TASALDPPEASA-----LPAALAVISFLGLGLGVAC 252  
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Search completed: August 3, 2004, 13:47:49  
 Job time : 26.8374 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2004, 13:01:34 ; Search time 7.59249 Seconds  
(without alignments)  
1754.300 Million cell updates/sec

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Perfect score: 1317  
Sequence: 1 MNRGVPRHLLVQLALP.....VISFLGLGVACVLRTR 258

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 125 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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50	1015	77.1	458	6 5223394-7	Patent No. 5223394
51	1012	76.8	334	3 US-08-328-500-2	Sequence 2, Appli
52	1012	76.8	334	3 US-08-466-368-2	Sequence 2, Appli
53	1003	76.2	394	6 5223418-2	Patent No. 5223418
54	916	69.6	434	1 US-08-236-311-4	Sequence 4, Appli
55	916	69.6	434	3 US-08-457-918-4	Sequence 4, Appli
56	914	69.4	410	3 US-08-630-172-17	Sequence 17, Appli
57	914	69.4	410	3 US-09-375-419-17	Sequence 17, Appli
58	899	68.3	433	3 US-09-100-409A-1	Sequence 1, Appli
59	899	68.3	903	1 US-08-021-601-12	Sequence 12, Appli
60	899	68.3	903	1 US-08-082-849B-12	Sequence 12, Appli
61	899	68.3	903	5 PCT-US94-01624-12	Sequence 12, Appli
62	898	68.2	433	2 US-08-867-149-1	Sequence 1, Appli
63	898	68.2	433	2 US-08-808-374-1	Sequence 1, Appli
64	718	54.5	433	6 517838-13	Patent No. 517838
65	716	54.4	138	3 US-08-630-172-1	Sequence 1, Appli
66	716	54.4	138	3 US-09-375-419-1	Sequence 1, Appli
67	595.5	45.2	376	2 US-08-558-269-10	Sequence 10, Appli
68	595.5	45.2	376	3 US-09-410-882-10	Sequence 10, Appli
69	589.5	44.8	383	2 US-08-558-269-6	Sequence 6, Appli
70	589.5	44.8	383	3 US-09-410-882-6	Sequence 6, Appli
71	494	37.5	94	3 US-08-466-368-5	Sequence 5, Appli
72	494	37.5	94	4 US-08-470-998-2	Sequence 2, Appli
73	494	37.5	94	4 US-08-328-500-10	Sequence 10, Appli
74	490.5	37.2	457	1 US-08-416-478A-8	Sequence 8, Appli
75	490.5	37.2	457	2 US-08-474-888B-8	Sequence 8, Appli
76	490.5	37.2	457	2 US-08-394-442B-8	Sequence 8, Appli
77	398	30.2	80	2 US-08-332-622A-84	Sequence 84, Appli
78	392	29.8	74	4 US-09-050-861B-8	Sequence 20, Appli
79	314	23.8	61	3 US-09-100-409A-20	Sequence 35, Appli
80	288	21.9	58	2 US-08-284-391B-35	Sequence 35, Appli
81	288	21.9	58	3 US-09-218-950-35	Sequence 35, Appli
82	228	17.3	46	3 US-09-100-409A-10	Sequence 10, Appli
83	228	17.3	81	3 US-09-100-409A-34	Sequence 34, Appli
84	212	16.1	154	3 US-08-630-172-7	Sequence 7, Appli
85	212	16.1	154	3 US-09-375-419-7	Sequence 7, Appli
86	211	16.0	40	3 US-09-100-409A-2	Sequence 2, Appli
87	211	16.0	42	3 US-09-100-409A-4	Sequence 4, Appli
88	211	16.0	77	3 US-09-100-409A-32	Sequence 32, Appli
89	200	15.2	41	6 5510256-5	Patent No. 5510256
90	168.5	12.8	81	2 US-08-332-622A-85	Sequence 85, Appli
91	167.5	12.7	81	2 US-08-332-622A-86	Sequence 86, Appli
92	167	12.7	34	3 US-09-100-409A-11	Sequence 11, Appli
93	167	12.7	39	3 US-09-100-409A-33	Sequence 33, Appli
94	156	11.8	29	3 US-09-100-409A-19	Sequence 19, Appli
95	151.5	11.5	47	3 US-09-303-323-92	Sequence 92, Appli
96	151.5	11.5	47	3 US-09-303-323-92	Sequence 92, Appli
97	151.5	11.5	47	4 US-09-770-014-92	Sequence 92, Appli
98	150	11.4	28	3 US-09-100-409A-3	Sequence 3, Appli
99	150	11.4	30	3 US-09-100-414B-91	Sequence 91, Appli
100	150	11.4	30	3 US-09-100-409A-5	Sequence 5, Appli

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101 150 11.4 30 3 US-09-303-323-91 Sequence 91, Appl
102 150 11.4 30 3 US-09-770-014-91 Sequence 91, Appl
103 150 11.4 47 3 US-09-100-414B-93 Sequence 93, Appl
104 150 11.4 47 3 US-09-100-414B-94 Sequence 94, Appl
105 150 11.4 47 3 US-09-100-409A-60 Sequence 60, Appl
106 150 11.4 47 3 US-09-303-323-93 Sequence 93, Appl
107 150 11.4 47 3 US-09-303-323-94 Sequence 94, Appl
108 150 11.4 47 3 US-09-770-014-93 Sequence 93, Appl
109 150 11.4 47 3 US-09-770-014-94 Sequence 94, Appl
110 150 11.4 50 3 US-09-100-409A-37 Sequence 37, Appl
111 144 10.9 64 3 US-09-100-409A-35 Sequence 35, Appl
112 139 10.6 25 6 5171838-24 Patent No. 5171838
113 133 10.1 25 6 5171838-23 Patent No. 5171838
114 131 9.9 1260 4 US-08-506-296B-21 Sequence 21, Appl
115 129 9.8 308 2 US-08-414-657D-46 Sequence 46, Appl
116 129 9.8 325 2 US-08-414-657D-2 Sequence 2, Appl
117 129 9.8 325 2 US-08-414-657D-41 Sequence 41, Appl
118 129 9.8 325 2 US-09-135-080-2 Sequence 2, Appl
119 129 9.8 338 2 US-08-414-657D-60 Sequence 60, Appl
120 129 9.8 338 4 US-09-135-080-8 Sequence 8, Appl
121 129 9.8 338 4 US-09-976-594-404 Patent No. 5171838
122 127 9.6 24 6 5171838-22 Patent No. 5171838
123 126 9.6 315 2 US-08-414-657D-47 Sequence 47, Appl
124 126 9.6 338 2 US-08-414-657D-42 Sequence 42, Appl
125 126 9.6 338 2 US-08-414-657D-43 Sequence 43, Appl
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## ALIGNMENTS

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RESULT 1
US-08-477-460B-6
; Sequence 6, Application US/08477460B
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,460B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
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; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-477-460B-6
Query Match 78.8%; Score 1038; DB 3; Length 310;
Best Local Similarity 85.7%; Pred. No. 3.5e-80;
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

1 MNRGVPFRLLLVLTALIPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKSNQIK 60
1 MNRGVPFRLLLVLTALIPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKSNQIK 60
1 IINGGSPFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNIKIDSDTYICEVEDQKEEYOL 120
61 IINGGSPFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNIKIDSDTYICEVEDQKEEYOL 120
121 LVFGLTANSDDLTLGQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
121 LVFGLTANSDDLTLGQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
181 TWTCYVLQKQKVEFEKIDIVPRASALPAPPTGSALPDPTASALDPDPAASALPALAVI 240
181 TWTCYVLQKQKVEFEKIDIVLAFTVAAP-----SVFIFFPSDEQLKSGTASV 228
241 SEFL 244
Db 229 VCLL 232

RESULT 2
US-08-379-516-6
; Sequence 6, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
; APPLICANT: Allaway, Graham P.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: No. 6083478 -Peptidy1 Moieety-Conjugated CD4-Gamma2 and CD4-19G2
; TITLE OF INVENTION: Immunconjugates and Uses Thereof
; FILE REFERENCE: 41215-A-PCT-US
; CURRENT APPLICATION NUMBER: US/08/379,516
; CURRENT FILING DATE: 1996-06-10
; EARLIER APPLICATION NUMBER: PCT/US93/07422
; EARLIER FILING DATE: 1993-08-06
; EARLIER APPLICATION NUMBER: 07/927,931
; EARLIER FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-379-516-6
Query Match 78.8%; Score 1038; DB 3; Length 310;
Best Local Similarity 85.7%; Pred. No. 3.5e-80;
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

1 MNRGVPFRLLLVLTALIPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKSNQIK 60
1 MNRGVPFRLLLVLTALIPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKSNQIK 60
1 IINGGSPFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNIKIDSDTYICEVEDQKEEYOL 120
61 IINGGSPFLTKGSPSKLNDRAISRSLMDQGNFPLIIKNIKIDSDTYICEVEDQKEEYOL 120
121 LVFGLTANSDDLTLGQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
121 LVFGLTANSDDLTLGQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
181 TWTCYVLQKQKVEFEKIDIVPRASALPAPPTGSALPDPTASALDPDPAASALPALAVI 240
181 TWTCYVLQKQKVEFEKIDIVLAFTVAAP-----SVFIFFPSDEQLKSGTASV 228
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QY 241 SFLL 244  
DB 229 VCLL 232

RESULT 3  
US-09-329-916-6  
Sequence 6, Application US/09329916  
Patent No. 6177549  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/329,916  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,460  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPM/AJM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-09-329-916-6

Query Match 78.8%; Score 1038; DB 3; Length 310;  
Best Local Similarity 85.7%; Pred. No. 3.5e-80;  
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;  
QY 1 MNRGVPRHLLVQLALLPAATQGNKVVGLKGGDTVELTCTASOKKSIOFHMKNNSQIK 60  
DB 1 MNRGVPRHLLVQLALLPAATQGNKVVGLKGGDTVELTCTASOKKSIOFHMKNNSQIK 60  
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
QY 121 LVFGLTANSSTHLLQGGSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSSTHLLQGGSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 121 LVFGLTANSSTHLLQGGSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSSTHLLQGGSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCVTVLQNGKVKVEFKIDIVPRASALPAPPTGSALPDQGTASALPDPPAASALPALAVI 240

DB 181 TWTCVTVLQNGKVKVEFKIDIVPRASALPAPPTGSALPDQGTASALPDPPAASALPALAVI 228  
QY 241 SFLL 244  
DB 229 VCLL 232

RESULT 4  
US-08-485-372A-6  
Sequence 6, Application US/08485372A  
Patent No. 6187748  
GENERAL INFORMATION:  
APPLICANT: Beaudry, Gary A.  
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,372A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,227  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 37690-II-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-485-372A-6

Query Match 78.8%; Score 1038; DB 3; Length 310;  
Best Local Similarity 85.7%; Pred. No. 3.5e-80;  
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;  
QY 1 MNRGVPRHLLVQLALLPAATQGNKVVGLKGGDTVELTCTASOKKSIOFHMKNNSQIK 60  
DB 1 MNRGVPRHLLVQLALLPAATQGNKVVGLKGGDTVELTCTASOKKSIOFHMKNNSQIK 60  
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
QY 121 LVFGLTANSSTHLLQGGSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSSTHLLQGGSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 121 LVFGLTANSSTHLLQGGSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTANSSTHLLQGGSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCVTVLQNGKVKVEFKIDIVPRASALPAPPTGSALPDQGTASALPDPPAASALPALAVI 240

Db 181 TWCTCTVLQNKQKVEFKIDIVLAFVTAAP-----SVFIFFPSDEQLKSGTASV 228  
QY 241 SFLL 244  
Db 229 VCILL 232

## RESULT 5

US-09-409-006A-6  
Sequence 6, Application US/09409006A  
Patent No. 6342586  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/409,006A  
FILING DATE: 29-SEP-1999  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-09-409-006A-6

Query Match 78.8%; Score 1038; DB 4; Length 310;  
Best local Similarity 85.7%; Pred. No. 3,5e-80;

Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 MNRGVFRRHLVLTQLALPAATGKRVLGKKGDTVELTCTASOKKSIQFHWKNSNOIK 60  
Db 1 MNRGVFRRHLVLTQLALPAATGKRVLGKKGDTVELTCTASOKKSIQFHWKNSNOIK 60  
QY 61 ILGNQGSFLTKGPKSKLNDRAISRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
Db 61 ILGNQGSFLTKGPKSKLNDRAISRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
QY 121 LVFGLTANSPTHLQOGSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
Db 121 LVFGLTANSPTHLQOGSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
QY 181 TWCTCTVLQNKQKVEFKIDIVPRASALPAPTGSALPDPTASALPDPASALPALAVI 240

Db 181 TWCTCTVLQNKQKVEFKIDIVLAFVTAAP-----SVFIFFPSDEQLKSGTASV 228  
QY 241 SFLL 244  
Db 229 VCILL 232

## RESULT 6

US-08-484-681-6  
Sequence 6, Application US/08484681  
Patent No. 6451313  
GENERAL INFORMATION:  
APPLICANT: Beaudry, Gary A.  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,681  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 37690-II-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-484-681-6

Query Match 78.8%; Score 1038; DB 4; Length 310;  
Best local Similarity 85.7%; Pred. No. 3,5e-80;

Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 MNRGVFRRHLVLTQLALPAATGKRVLGKKGDTVELTCTASOKKSIQFHWKNSNOIK 60  
Db 1 MNRGVFRRHLVLTQLALPAATGKRVLGKKGDTVELTCTASOKKSIQFHWKNSNOIK 60  
QY 61 ILGNQGSFLTKGPKSKLNDRAISRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
Db 61 ILGNQGSFLTKGPKSKLNDRAISRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120  
QY 121 LVFGLTANSPTHLQOGSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
Db 121 LVFGLTANSPTHLQOGSLTTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
QY 181 TWCTCTVLQNKQKVEFKIDIVPRASALPAPTGSALPDPTASALPDPASALPALAVI 240  
Db 181 TWCTCTVLQNKQKVEFKIDIVLAFVTAAP-----SVFIFFPSDEQLKSGTASV 228

Qy 241 SFL 244  
Db 229 VCLL 232

RESULT 7  
PCT-US93-07422-6  
Sequence 6, Application PC/TUS9307422  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07422  
FILING DATE: 19930806  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 310 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
PCT-US93-07422-6

Query Match 78.8%; Score 1038; DB 5; Length 310;  
Best Local Similarity 85.7%; Pred. No. 3.5e-80;  
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;  
Qy 1 MNRGVPFRHLLVLVQLALLPAATQGNKRVLGKGGDTVELTCTASQKKSIGFHMKNNSQIK 60  
Db 1 MNRGVPFRHLLVLVQLALLPAATQGNKRVLGKGGDTVELTCTASQKKSIGFHMKNNSQIK 60  
Qy 61 ILNQGSEFLTKGSKNDRAADRSRLMDQGNFPLIINKLTIKESDPTICVEEQKEVOL 120  
Db 61 ILNQGSEFLTKGSKNDRAADRSRLMDQGNFPLIINKLTIKESDPTICVEEQKEVOL 120  
Qy 121 LVEGLTANSPDTHLLQGSQSLTLTLESPPGSSPSVQCRRPRGKNIQGGKTLSSVQLELDGSG 180  
Db 121 LVEGLTANSPDTHLLQGSQSLTLTLESPPGSSPSVQCRRPRGKNIQGGKTLSSVQLELDGSG 180  
Qy 181 TWCTCTVQONQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
Db 181 TWCTCTVQONQKVEFKIDIVLAFTVAAP-----SVFIFFPSDEQLKSGTASV 228  
Qy 241 SFL 244

Db 229 VCLL 232

RESULT 8  
US-08-477-460B-2  
Sequence 2, Application US/08477460B  
Patent No. 6034223  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,460B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-477-460B-2

Query Match 78.4%; Score 1032.5; DB 3; Length 432;  
Best Local Similarity 88.0%; Pred. No. 1.6e-79;  
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;  
Qy 1 MNRGVPFRHLLVLVQLALLPAATQGNKRVLGKGGDTVELTCTASQKKSIGFHMKNNSQIK 60  
Db 1 MNRGVPFRHLLVLVQLALLPAATQGNKRVLGKGGDTVELTCTASQKKSIGFHMKNNSQIK 60  
Qy 61 ILNQGSEFLTKGSKNDRAADRSRLMDQGNFPLIINKLTIKESDPTICVEEQKEVOL 120  
Db 61 ILNQGSEFLTKGSKNDRAADRSRLMDQGNFPLIINKLTIKESDPTICVEEQKEVOL 120  
Qy 121 LVEGLTANSPDTHLLQGSQSLTLTLESPPGSSPSVQCRRPRGKNIQGGKTLSSVQLELDGSG 180  
Db 121 LVEGLTANSPDTHLLQGSQSLTLTLESPPGSSPSVQCRRPRGKNIQGGKTLSSVQLELDGSG 180  
Qy 181 TWCTCTVQONQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPA 230  
Db 181 TWCTCTVQONQKVEFKIDIVLAFFERKCCVECP-----CPAPVA 221

RESULT 9  
US-08-379-516-2  
Sequence 2, Application US/08379516  
Patent No. 6083478  
GENERAL INFORMATION:  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IGG2  
FILE REFERENCE: 41215-A-PCT-US  
CURRENT APPLICATION NUMBER: US/08/379,516  
EARLIER FILING DATE: 1996-06-10  
EARLIER APPLICATION NUMBER: PCT/US93/07422  
EARLIER FILING DATE: 1993-08-06  
EARLIER APPLICATION NUMBER: 07/927,931  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 432  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-379-516-2

Query Match 78.4%; Score 1032.5; DB 3; Length 432;  
Best Local Similarity 88.0%; Pred. No. 1.6e-79;  
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVFRRLLLVQLALPAATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNOIK 60  
DB 1 MNRGVFRRLLLVQLALPAATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNOIK 60  
QY 61 ILGNQGSFLTKGSPSKINDRADSRSLWDQGNFPLIINKIKIEDSDTYICEVEDQKEEVL 120  
DB 61 ILGNQGSFLTKGSPSKINDRADSRSLWDQGNFPLIINKIKIEDSDTYICEVEDQKEEVL 120  
QY 121 LVFGLTNSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTNSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCTVLQNKVKVEFKIDIV---PRASALPAPPTGSALPDPTASALPDPPAA 230  
DB 181 TWTCTVLQNKVKVEFKIDIVLAFERKCCVCECP-----CPAPVA 221

RESULT 10  
US-09-329-916-2  
Sequence 2, Application US/09329916  
Patent No. 6177549  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/329,916  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/477,460  
FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPM/AJM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-09-329-916-2

Query Match 78.4%; Score 1032.5; DB 3; Length 432;  
Best Local Similarity 88.0%; Pred. No. 1.6e-79;  
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVFRRLLLVQLALPAATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNOIK 60  
DB 1 MNRGVFRRLLLVQLALPAATQGNKVVLGKGGDTVELTCTASQKSIQFHMKNNOIK 60  
QY 61 ILGNQGSFLTKGSPSKINDRADSRSLWDQGNFPLIINKIKIEDSDTYICEVEDQKEEVL 120  
DB 61 ILGNQGSFLTKGSPSKINDRADSRSLWDQGNFPLIINKIKIEDSDTYICEVEDQKEEVL 120  
QY 121 LVFGLTNSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
DB 121 LVFGLTNSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180  
QY 181 TWTCTVLQNKVKVEFKIDIV---PRASALPAPPTGSALPDPTASALPDPPAA 230  
DB 181 TWTCTVLQNKVKVEFKIDIVLAFERKCCVCECP-----CPAPVA 221

RESULT 11  
US-08-485-372A-2  
Sequence 2, Application US/08485372A  
Patent No. 6187748  
GENERAL INFORMATION:  
APPLICANT: Beaudry, Gary A.  
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,372A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,227  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.



REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 37690-II-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-485-372A-2

Query Match 78.4%; Score 1032.5; DB 3; Length 432;  
Best Local Similarity 88.0%; Pred. No. 1.6e-79;  
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60  
DB 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60  
QY 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSPTHLIQGSLTLTLSPGSSPSVQCSPRGKNIQGGKTLSSVSOLELDGSG 180  
DB 121 LVFGLTANSPTHLIQGSLTLTLSPGSSPSVQCSPRGKNIQGGKTLSSVSOLELDGSG 180  
QY 181 TWICTVLQNKQKVEFKIDIV----PRASALPAPPTGSALPDPTASALPDPPAA 230  
DB 181 TWICTVLQNKQKVEFKIDIVLAERKCCVCECP-----CPAPPA 221

RESULT 12  
US-09-409-006A-2  
Sequence 2, Application US/09409006A  
Patent No. 6342586  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/409,006A  
FILING DATE: 29-SEP-1999  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550

TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-09-409-006A-2

Query Match 78.4%; Score 1032.5; DB 4; Length 432;  
Best Local Similarity 88.0%; Pred. No. 1.6e-79;  
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60  
DB 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60  
QY 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSPTHLIQGSLTLTLSPGSSPSVQCSPRGKNIQGGKTLSSVSOLELDGSG 180  
DB 121 LVFGLTANSPTHLIQGSLTLTLSPGSSPSVQCSPRGKNIQGGKTLSSVSOLELDGSG 180  
QY 181 TWICTVLQNKQKVEFKIDIV----PRASALPAPPTGSALPDPTASALPDPPAA 230  
DB 181 TWICTVLQNKQKVEFKIDIVLAERKCCVCECP-----CPAPPA 221

RESULT 13  
US-08-484-681-2  
Sequence 2, Application US/08484681  
Patent No. 6451313  
GENERAL INFORMATION:  
APPLICANT: Beaudry, Gary A.  
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,681  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 37690-II-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown

TOPOLOGY: unknown  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-484-681-2

Query Match 78.4%; Score 1032.5; DB 4; Length 432;  
Best Local Similarity 88.0%; Pred. No. 1.6e-79;  
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVFRRHLVLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNQIK 60  
DB 1 MNRGVFRRHLVLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNQIK 60  
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSDTHLQOGSLTLTLESPPGSSPSVQCSPPGKNIOGKTLVSQLELODSG 180  
DB 121 LVFGLTANSDTHLQOGSLTLTLESPPGSSPSVQCSPPGKNIOGKTLVSQLELODSG 180  
QY 181 TWICTVLQNKQKVEFKIDIV---PRASALPAPPTGSALPDPTASALPDPPAA 230  
DB 181 TWICTVLQNKQKVEFKIDIVLAERKCCVECP-----CPAPVA 221

## RESULT 14

PCT-US93-07422-2  
Sequence 2, Application PC/TUS9307422

GENERAL INFORMATION:

APPLICANT: Progenics Pharmaceuticals, Inc.

TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED

TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07422

FILING DATE: 19930806

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPM/AJM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 977-9809

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

ORGANISM: homo sapien

CELL TYPE: lymphocyte

PCT-US93-07422-2

Query Match 78.4%; Score 1032.5; DB 5; Length 432;  
Best Local Similarity 88.0%; Pred. No. 1.6e-79;  
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVFRRHLVLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNQIK 60  
DB 1 MNRGVFRRHLVLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNQIK 60  
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSDTHLQOGSLTLTLESPPGSSPSVQCSPPGKNIOGKTLVSQLELODSG 180  
DB 121 LVFGLTANSDTHLQOGSLTLTLESPPGSSPSVQCSPPGKNIOGKTLVSQLELODSG 180  
QY 181 TWICTVLQNKQKVEFKIDIV---PRASALPAPPTGSALPDPTASALPDPPAA 230  
DB 181 TWICTVLQNKQKVEFKIDIVLAERKCCVECP-----CPAPVA 221

## RESULT 15

US-08-477-460B-4  
Sequence 4, Application US/08477460B

Patent No. 6034223

GENERAL INFORMATION:

APPLICANT: Progenics Pharmaceuticals, Inc.

TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED

TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,460B

FILING DATE: 07-JUN-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPM/AJM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 977-9809

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 530 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: CDNA

ORGANISM: homo sapien

CELL TYPE: lymphocyte

US-08-477-460B-4

Query Match 78.2%; Score 1030.5; DB 3; Length 530;  
Best Local Similarity 84.8%; Pred. No. 3.1e-79;



RESULT 18  
US-08-485-372A-4  
; Sequence 4, Application US/08485372A  
; Patent No. 6187748  
; GENERAL INFORMATION:  
; APPLICANT: Beaudry, Gary A.  
; APPLICANT: Maddon, Paul J.  
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,372A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/476,227  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 37690-II-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 530 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapien  
; CELL TYPE: lymphocyte  
; US-08-485-372A-4

Query Match 78.2%; Score 1030.5; DB 3; Length 530;  
Best Local Similarity 84.8%; Pred. No. 3.1e-79;  
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;  
QY 1 MNRGVPFRHLVLVQLALPAATGKNVVLGKKGDTVELTCTASQKKSIOFHKNSNOIK 60  
Db 1 MNRGVPFRHLVLVQLALPAATGKNVVLGKKGDTVELTCTASQKKSIOFHKNSNOIK 60  
QY 61 ILGNQGSFLTKGSPKLNDRADSRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120  
Db 61 ILGNQGSFLTKGSPKLNDRADSRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCSPRGKNIOGKTLVSQLELODSG 180  
Db 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCSPRGKNIOGKTLVSQLELODSG 180  
QY 181 TWICTVLQKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
Db 181 TWICTVLQKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
QY 241 SFL 244  
Db 230 GCLV 233

RESULT 19  
US-09-409-006A-4  
; Sequence 4, Application US/09409006A  
; Patent No. 6342586  
; GENERAL INFORMATION:  
; APPLICANT: Progenice Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/409,006A  
; FILING DATE: 29-SEP-1999  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/927,931  
; FILING DATE: 07-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 977-9809  
; TELEX: 422523 COOP UI  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 530 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapien  
; CELL TYPE: lymphocyte  
; US-09-409-006A-4

Query Match 78.2%; Score 1030.5; DB 4; Length 530;  
Best Local Similarity 84.8%; Pred. No. 3.1e-79;  
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;  
QY 1 MNRGVPFRHLVLVQLALPAATGKNVVLGKKGDTVELTCTASQKKSIOFHKNSNOIK 60  
Db 1 MNRGVPFRHLVLVQLALPAATGKNVVLGKKGDTVELTCTASQKKSIOFHKNSNOIK 60  
QY 61 ILGNQGSFLTKGSPKLNDRADSRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120  
Db 61 ILGNQGSFLTKGSPKLNDRADSRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCSPRGKNIOGKTLVSQLELODSG 180  
Db 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCSPRGKNIOGKTLVSQLELODSG 180  
QY 181 TWICTVLQKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
Db 181 TWICTVLQKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
QY 241 SFL 244  
Db 230 GCLV 233

## RESULT 20

US-08-484-681-4  
Sequence 4, Application US/08484681  
Patent No. 6451313  
GENERAL INFORMATION:  
APPLICANT: Beaudry, Gary A.  
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,681  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 37690-II-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 530 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-484-681-4

Query Match 78.2%; Score 1030.5; DB 4; Length 530;  
Best Local Similarity 84.8%; Pred. No. 3.1e-79;

Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPRRLHLLVQLALPAAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60  
DB 1 MNRGVPRRLHLLVQLALPAAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60  
QY 61 ILNGQSFLLTKGSPSKLNDRAADRSRLMDQGNFPLIINKLTIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILNGQSFLLTKGSPSKLNDRAADRSRLMDQGNFPLIINKLTIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSPTHLTQGSLLTLESPPGSSPSVQCRRSPRGKNIQGGKTLSSVQLELDQSG 180  
DB 121 LVFGLTANSPTHLTQGSLLTLESPPGSSPSVQCRRSPRGKNIQGGKTLSSVQLELDQSG 180  
QY 181 TWTCTVLOQOKKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
DB 181 TWTCTVLOQOKKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
QY 241 SFL 244  
DB 230 GCLV 233

RESULT 21  
PCT-US93-07422-4

Sequence 4, Application PC/TUS9307422  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07422  
FILING DATE: 19930806  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UT  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 530 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
PCT-US93-07422-4

Query Match 78.2%; Score 1030.5; DB 5; Length 530;  
Best Local Similarity 84.8%; Pred. No. 3.1e-79;

Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPRRLHLLVQLALPAAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60  
DB 1 MNRGVPRRLHLLVQLALPAAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60  
QY 61 ILNGQSFLLTKGSPSKLNDRAADRSRLMDQGNFPLIINKLTIEDSDTYICEVEDQKEEVOL 120  
DB 61 ILNGQSFLLTKGSPSKLNDRAADRSRLMDQGNFPLIINKLTIEDSDTYICEVEDQKEEVOL 120  
QY 121 LVFGLTANSPTHLTQGSLLTLESPPGSSPSVQCRRSPRGKNIQGGKTLSSVQLELDQSG 180  
DB 121 LVFGLTANSPTHLTQGSLLTLESPPGSSPSVQCRRSPRGKNIQGGKTLSSVQLELDQSG 180  
QY 181 TWTCTVLOQOKKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
DB 181 TWTCTVLOQOKKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240  
QY 241 SFL 244  
DB 230 GCLV 233

RESULT 22  
US-08-284-391B-31  
Sequence 31, Application US/08284391B

```
Patent No. 5851828
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-284-391B-31

Query Match      78.1%; Score 1029; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 1,1e-79;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60
DB 1 MNRGVPRHLLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60
QY 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQL 120
DB 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQL 120
QY 121 LVFGLTANSPTHLIQGQSLTLTLESPGSSPSVQCRSPRGKNTQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLIQGQSLTLTLESPGSSPSVQCRSPRGKNTQGGKTLVSQLELDQSG 180
QY 181 TWCTCTVLQNKQKVEFKIDIV 200
DB 181 TWCTCTVLQNKQKVEFKIDIV 200

RESULT 23
US-09-218-950-31
Sequence 31, Application US/09218950
```

```
Patent No. 6284240
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,950
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-218-950-31

Query Match      78.1%; Score 1029; DB 3; Length 203;
Best Local Similarity 100.0%; Pred. No. 1,1e-79;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60
DB 1 MNRGVPRHLLVQLALPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNSQIK 60
QY 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQL 120
DB 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQL 120
QY 121 LVFGLTANSPTHLIQGQSLTLTLESPGSSPSVQCRSPRGKNTQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLIQGQSLTLTLESPGSSPSVQCRSPRGKNTQGGKTLVSQLELDQSG 180
QY 181 TWCTCTVLQNKQKVEFKIDIV 200
DB 181 TWCTCTVLQNKQKVEFKIDIV 200

RESULT 24
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US-08-284-391B-29  
Sequence 29, Application US/08284391B  
Patent No. 5851828  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian  
APPLICANT: Banapour, Babak  
APPLICANT: Romeo, Charles  
APPLICANT: Kolanus, Waldemar  
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED  
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,391B  
FILING DATE: 02-AUG-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/195,395  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: 07/847,566  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/665,961  
FILING DATE: 07-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Elbing, Karen L  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/247001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 398 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-284-391B-29

Query Match 78.1%; Score 1029; DB 2; Length 398;  
Best Local Similarity 100.0%; Pred. No. 2.8e-79;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLLVQLALLPAATGKNVVLGKGGDTVELTCTASOKSIOFHMNSNOIK 60  
DB 1 MNRGVPFRHLLVQLALLPAATGKNVVLGKGGDTVELTCTASOKSIOFHMNSNOIK 60  
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINLKIETSDTYICEVEDQKEVOL 120  
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINLKIETSDTYICEVEDQKEVOL 120  
QY 121 LVFGLTANSPTHLLOGSGLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
DB 121 LVFGLTANSPTHLLOGSGLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
QY 121 LVFGLTANSPTHLLOGSGLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
DB 121 LVFGLTANSPTHLLOGSGLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
QY 181 TWTCTVLONOKKVEFKIDIV 200  
DB 181 TWTCTVLONOKKVEFKIDIV 200

RESULT 25

US-09-218-950-29  
Sequence 29, Application US/09218950  
Patent No. 6284240  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian  
APPLICANT: Banapour, Babak  
APPLICANT: Romeo, Charles  
APPLICANT: Kolanus, Waldemar  
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED  
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/218,950  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,391  
FILING DATE: 02-AUG-1994  
APPLICATION NUMBER: 08/195,395  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: 07/847,566  
FILING DATE: 06-MAR-1992  
APPLICATION NUMBER: 07/665,961  
FILING DATE: 07-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Elbing, Karen L  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/247001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 398 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-218-950-29

Query Match 78.1%; Score 1029; DB 3; Length 398;  
Best Local Similarity 100.0%; Pred. No. 2.8e-79;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLLVQLALLPAATGKNVVLGKGGDTVELTCTASOKSIOFHMNSNOIK 60  
DB 1 MNRGVPFRHLLVQLALLPAATGKNVVLGKGGDTVELTCTASOKSIOFHMNSNOIK 60  
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINLKIETSDTYICEVEDQKEVOL 120  
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINLKIETSDTYICEVEDQKEVOL 120  
QY 121 LVFGLTANSPTHLLOGSGLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
DB 121 LVFGLTANSPTHLLOGSGLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
QY 121 LVFGLTANSPTHLLOGSGLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
DB 121 LVFGLTANSPTHLLOGSGLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180  
QY 181 TWTCTVLONOKKVEFKIDIV 200  
DB 181 TWTCTVLONOKKVEFKIDIV 200

```
RESULT 26
US-08-236-311-1
; Sequence 1, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Haasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-236-311-1

Query Match      78.1%; Score 1029; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.8e-79;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALLPAATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNNSQIK 60
DB 1 MNRGVPRHLLVQLALLPAATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNNSQIK 60
QY 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSQSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSQSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200
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RESULT 27
US-08-457-918-1
; Sequence 1, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-457-918-1

Query Match      78.1%; Score 1029; DB 3; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.8e-79;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALLPAATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNNSQIK 60
DB 1 MNRGVPRHLLVQLALLPAATQGNKVVLGKKGDVVELTCTASQKKSIOFHMKNNSQIK 60
QY 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSQSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSQSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200
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